

seq name: /SIND1/acgdata/geneseq/geneseq/NA2001.DAT:AAD04547

```
seq_documentation_block:
ID: AAD04547 standard; cDNA; 426 BP.
XX
XX AAD04547;
XX
XX 17-JUL-2001 (first entry)
DT
```

XX Homo sapiens.

XX  
CC  
nono  
paf  
:one

FH	Key	Location/Qualifiers
----	-----	---------------------

```
FT      CDS
FT      1..426
FT      /*tag= a
FT      /product= "Novel human protein (NHP) #1 which share
```

```
FT / *tag= d
FT /product= "Novel human protein (NHP) #1 which share
```

FT  
FT  
sequen

FT	sig_peptide	1..96
----	-------------	-------

ET

```

FT mat_peptide
9/..42
/*tag=

```

	FT	/prod	/cas
FT			
/prod			
/cas			

XX

PN WO200127273-A1.

XX  
19-APR-2001XX  
ED AFN 2001.

PF 10-OCT-2000; 2000WO-US

XX XX

PR 12-OCT-1999; 9905-01  
VY

PA (LEXI-) LEXICON GENETI

XX XX

PI Turner CA, Donoho G,

XX WPT: 2001-300218/31

DR WFL, 2001 300210/34.  
DR P-PSDB: AAE01017.

XX  
XX  
XX

PT New nucleic acid sequen

galanin family, user

XX  
If it is possible to find a way to make the...

PS Claim 1; Page 25; 29pp

XX

cc The present sequence

cc which charac sequence

CC which shares sequence  
CC biologically active pe

peripheral nervous sys

CC in response to oestrogen

CC, clinical trial monitor

CC imbalance. Galanin modulates body weight

repair, Alzheimer's de

CC disease.

XX XX

SQ Sequence 426 BP; 10/

alignment\_scores:

Quality: 734.0

\_\_\_\_\_



117 rGlyArgGlnSerLeuGluAspValLeuGlyMetLeuSerMetLysIleProL 134  
 295 .....

134 ysGluGluAspValLeuLysSer 141  
 326 AGGAGGAAGATGCTCTGAAGTCA 348

seq\_name: /SIDS1/gcgdata/geneseq/geneseq/NA1999.DAT:AAZ25536

seq\_documentation\_block:

ID AAZ25536 standard; cDNA; 473 BP.

AC AAZ25536;

DT 21-DEC-1999 (first entry)

DE Receptor binding peptide encoding cDNA SEQ ID NO:42.

XX Physiologically active peptide; receptor binding; galanin receptor;  
 KW GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin;  
 KW drug development; memory function; appetite improver; womb; kidney;  
 KW function regulator; prostate; testis; skeletal muscle; ss.

XX Homo sapiens.

OS WO9948920-A1.

PN 30-SEP-1999.

PD 24-MAR-1999; 99WO-JP01482.

PF 25-MAR-1998; 98JP-0078139.

PR 21-SEP-1998; 98JP-0266972.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Ohtaki T, Matsui H, Ishibashi Y, Ogi K, Kitada C;

XX WPI; 1999-572170/48.

XX Peptides binding to galanin receptor proteins, used to, e.g. improve  
 PT kidney functioning -

XX Claim 13; Page 143; 153pp; Japanese.

XX The present invention describes peptides (I) binding to galanin receptor  
 CC proteins. (I) contain the sequence APAHRGRGG or one substantially  
 CC identical to it, and their precursors, salts, amides and esters, which  
 CC bind especially to rat galanin receptor proteins. Products from the  
 CC present invention are used in assays of galanin/galanin receptor binding  
 CC and the development of drugs acting on galanin binding, such as memory  
 CC function improvers, appetite improvers, and function regulators for the  
 CC womb, kidney, prostate, testis or skeletal muscle. AAY45129 to AAY45154  
 CC and AAZ25518 to AAZ25552 represent sequences used in the exemplification  
 CC of the present invention.

XX Sequence 473 BP; 96 A; 155 C; 124 G; 98 T; 0 other;

alignment\_scores:

Quality: 580.50 Length: 141  
 Ratio: 5.004 Gaps: 1  
 Percent Similarity: 82.270 Percent Identity: 82.270

alignment\_block:

US-09-689-911-2 x AAZ25536 ..

Align seg 1/1 to: AAZ25536 from: 1 to: 473

1 MetAlaProSerValProLeuValLeuLeuValLeuLeuSe 17  
 |||

83 ATGGCTCCTCCTCGTCCCGTCCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTGAG 132  
 17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34  
 133 CTGGCAGAGACTCCAGCATCCGACCTGCCACCGGGGAGGAGGCT 182  
 34 rpThrLeuAsnSerAlaGlyThrLeuLeuGlyProValLeuHisLeuPro 50  
 183 GGACCTCAATAGTGTGCTGCTACCTTCTGGGTCCCTCCTCCTCCTCCTCCTCC 232  
 51 GlnMetGlyAspGlnAspGlyLysArgGluThrAlaLeuGluIleLeuAs 67  
 233 CAATGGGTGACCAAGACGAAAGAGGAGACAGCCCTTGAGATCCTAGA 282  
 67 pLeuTrpLysAlaIleAspGlyLeuProTySerHisProGlnProS 84  
 283 CCTGTGGAGGCCATCGATGGCTCCCTTACTCCACCCCTCCACAGCCCT 332  
 84 erLysArgAsnValMetGluThrPheAlaLysProGluIleGlyGlyLys 100  
 333 CCAGAGGAATGTGATGGAGAGCTTTGCCAACCAGAGATTGA..... 376  
 101 AlaArgLysHisArgArgGluThrProThrGlyGluGlyGluGlnGlySe 117  
 376 ..... 376  
 117 rGlyArgGlnSerLeuGluAspValLeuGlyMetLeuSerMetLysIleProL 134  
 377 .....GATCTGGGCATGCTCAGCATGAATAATTCCTCA 407

134 ysGluGluAspValLeuLysSer 141  
 408 AGGAGGAAGATGCTCTGAAGTCA 430

seq\_name: /SIDS1/gcgdata/geneseq/geneseq/NA1999.DAT:AAZ25535

seq\_documentation\_block:

ID AAZ25535 standard; cDNA; 695 BP.

AC AAZ25535;

DT 21-DEC-1999 (first entry)

DE Receptor binding peptide encoding cDNA SEQ ID NO:41.

XX Physiologically active peptide; receptor binding; galanin receptor;  
 KW GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin;  
 KW drug development; memory function; appetite improver; womb; kidney;  
 KW function regulator; prostate; testis; skeletal muscle; ss.

XX Rattus sp.

XX WO9948920-A1.

XX 30-SEP-1999.

XX 24-MAR-1999; 99WO-JP01482.

XX 25-MAR-1998; 98JP-0078139.

XX 21-SEP-1998; 98JP-0266972.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Ohtaki T, Matsui H, Ishibashi Y, Ogi K, Kitada C;

XX WPI; 1999-572170/48.

XX Peptides binding to galanin receptor proteins, used to, e.g. improve  
 PT kidney functioning -

XX Claim 13; Page 143; 153pp; Japanese.

XX The present invention describes peptides (I) binding to galanin receptor

PN	WO9948920-A1.	
XX		
PD	30-SEP-1999.	
XX		
PF	24-MAR-1999; 99WO-JP01482.	
XX		
XX	25-MAR-1998; 98JP-0078139.	
PR	21-SEP-1998; 98JP-0266972.	
XX		
PA	(TAKE ) TAKEDA CHEM IND LTD.	
XX		
PI	Ohtaki T, Matsui H, Ishibashi Y, Ogi K, Kitada C;	
XX		
DR	WPI; 1999-572170/48.	
DR	P-PSDB; AAY45143.	
XX		
PT	Peptides binding to galanin receptor proteins, used to, e.g. improve	
PT	kidney functioning -	
XX		
PS	Claim 13; Page 135; 153pp; Japanese.	
XX		
CC	The present invention describes peptides (I) binding to galanin receptor	
CC	proteins. (I) contain the sequence APAHRGRGG or one substantially	
CC	identical to it, and their precursors, salts, amides and esters, which	
CC	bind especially to rat galanin receptor proteins, products from the	
CC	present invention are used in assays of galanin/galanin receptor binding	
CC	and the development of drugs acting on galanin binding, such as memory	
CC	function improvers, appetite improvers, and function regulators for the	
CC	womb, kidney, prostate, testis or skeletal muscle. AAY45129 to AAY45154	
CC	and AAY25518 to AAY25552 represent sequences used in the exemplification	
CC	of the present invention.	

PA (TAKE ) TAKEDA CHEM IND LTD.  
XX

XX  
DP WPT: 1000-572170/10

DR WFL; 1999-5/21/0/48.  
DR P-PSDB; AAY45143.  
XX  
PT peptides binding to galanin receptor proteins used to improve

PT kidney functioning -  
yy

XX  
PS  
Claim 13. Page 135. 153no. Japanese

The present invention describes methods and systems

proteins. (I) contain the sequence APAHRGG or one substantially identical to it and their precursors salts amides and esters which

CC bind especially to rat galanin receptor proteins. Products from the  
CC identical to it, and their precursors, salts, amides and esters, which  
CC bind especially to rat galanin receptor proteins. Products from the  
CC present invention are used in assays of galanin/galanin receptor binding

CC and the development of drugs acting on galanin binding, such as memory  
CC function improvers, appetite improvers and function regulators for the

womb, kidney, prostate, testis or skeletal muscle. AAY45129 to AAY45154  
CC and AAZ25518 to AAZ25552 represent sequences used in the emm1ification  
CC

CC of the present invention.  
XX

Sequence 974 BP; 258 A; 278 C; 229 G; 209 T; 0 other;

alignment scores.

alignment_scores:		
Quality:	342.00	Length: 140
Ratio:	3.320	Gaps: 5

Percent Similarity: 73.571    Percent Identity: 57.857

```
alignment_block:
US-09-689-911-2 x AA225530
```

Align seq 1/1 to: AA725530 from: 1 to: 974

```
align seg 1/1  to: AA425550 from: 1 to: 5/4
5 serval|profeiva|ten|ten|en|va|ten|ten|en|sen|ten|a|a|cl|uth 21
```

[illegible]

44 ACAGGCCCTCAGATCGTCTTGGAGTC...CTGGCTCAGCGCTGATGGAGTC 90

[illegible]

51 TCCAGGCTTCGTCGGGTCCACAGGGGGCGAGGAGGCTGGAGCCCTCAACA 140

38 eRAIaCIvTvIenIenCIvproValIenIuIisIenproCIenMetCIvAsn 54

[illegible]

F  
F  
F  
E  
F  
F  
F  
C  
C  
F  
F  
E  
C  
C  
C  
C  
C  
C  
C

55 GlnAspGlyLysArgGluThrAlaLeuGluIleLeuAspLeuTrpLysAl 71

191 GGAGCGGGAAGGGAAGACACAGCCCTCGGGATCCTGGACCTGTGGAAGC 240

ALL INFORMATION CONTAINED HEREIN IS UNCLASSIFIED

71 aileAspGlyLeuProTyrSerHisProGlnProSerLysArgAsnV 88

1  
 2  
 3  
 4  
 5  
 6  
 7  
 8  
 9  
 10  
 11  
 12  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400  
 401  
 402  
 403  
 404  
 405  
 406  
 407  
 408  
 409  
 410  
 411  
 412  
 413  
 414  
 415  
 416  
 417  
 418  
 419  
 420  
 421  
 422  
 423  
 424  
 425  
 426  
 427  
 428  
 429  
 430  
 431  
 432  
 433  
 434  
 435  
 436  
 437  
 438  
 439  
 440  
 441  
 442  
 443  
 444  
 445  
 446  
 447  
 448  
 449  
 450  
 451  
 452  
 453  
 454  
 455  
 456  
 457  
 458  
 459  
 460  
 461  
 462  
 463  
 464  
 465  
 466  
 467  
 468  
 469  
 470  
 471  
 472  
 473  
 474  
 475  
 476  
 477  
 478  
 479  
 480  
 481  
 482  
 483  
 484  
 485  
 486  
 487  
 488  
 489  
 490  
 491  
 492  
 493  
 494  
 495  
 496  
 497  
 498  
 499  
 500  
 501  
 502  
 503  
 504  
 505  
 506  
 507  
 508  
 509  
 510  
 511  
 512  
 513  
 514  
 515  
 516  
 517  
 518  
 519  
 520  
 521  
 522  
 523  
 524  
 525

241 CATTGAAGGGCTCCCGCATATCCCAAGTCTCAGTTGGCCCTCCAAGAGGATC 290

88 aMetGlutThrPheAlaLysProGluIleGlyGlyLysAlaArgLys.Hi 104  
:: |||||  
291 TGGGGGAGACTTCGCCAACACAGACTCTGGA.....GTAAACA 328  
|||

104 sArqArqGluThrProThr.GluGluGluGluGlnGlnGlnSerGluVArqGln 120

[illegible]

329 TTTGTGGAGTTCCTGACGTGGTGGTGGAAACGAATCCGACCAGGAAC 378

41 rLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnaspGlyL 58  
 |||||  
 51 CCYTCTGGGTCGGTCTCTCACTTCCCAATGGTGACCAAGACGGAA 100  
 |||||  
 58 ysArgGlnThrAlaLeuGluIleLeuAspLeuTrpLysAlaIleaspGly 74  
 |||||  
 101 AGAGGGNAGACGCCCTTGAGATCCTAGACTGTGGAAGGCCATCGATGGG 150  
 |||||  
 75 LeuProTyrSerHisProGlnProSer 84  
 |||||  
 1 CTCCCTACTCCACCGCTCCACACGGCTCC 180

```

-- name: /snp1/acadata/geneseq/geneseq/NA2001.DAT:AAF44071

```

```
seq_documentation_block:
ID AAF44071 standard; DNA; 180 BP.
XX
XX AAF44071.
```

XX receptor binding peptide encoding cDNA SEQ ID NO:40.

23-MAR-2001 (first entry)  
DNA encoding a human physiologically active protein.  
Physiologically active protein; galanin receptor; GALR; FGF;  
fibroblast growth factor; ds.

XX	WC9948920-A1	XX	nama panjang
DN		CC	

XX	30-SEP-1999.	XX	JP20000270871-A.
PD		DN	

XX	24-MAR-1999:	99WO-JP01482.	XX	01-2000-2000.
PF			PF	03-OCT-2000.

[illegible]

FR	23 MAR 1999	XX	24 MAR 1999
PR	21-SEP-1998;	XX	21-SEP-1998;
	98JP-0266972.		

XX	PA	(TAKE ) TAKEDA CHEM IND LTD.	PR	XX
XX			24-MAR-1999	XX

XX	PI	Ohtaki T, Matsui H, Ishibashi Y, Ogi K, Kitada C;	PA (TAKE ) TAKE XX
----	----	---	--------------------------

XX	WPI; 1999-572170/48.	DR	WPI; 2001-01
XX		XX	

peptides binding to galanin receptor proteins, used to, e.g. improve

XX	PS	claim 11; page 142; 153pp; Japanese.	PS	disclosure;
XX	XX		XX	

CC The present invention describes peptides (I) binding to gamma receptors.

CC proteins. (I) contain the sequence APAHRGRGG or one substantially

CC physiological and N-terminal

bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding

CC function improvers, appetite improvers, and function regulators for the CC and the development of drugs acting on gamma-aminobutyric acid (GABA) receptors. CC sequences AAY45129 to AAY45154 used in the CC

CC	and AA225518 to AA225552 represent sequences used in the exemplification	XX
CC	of the present invention.	SO
		Sequence 18

SQ Sequence 180 BP; 37 A; 66 C; 47 G; 30 T; 0 other;

alignment_scores:	length:	Qual	Ra
60	60	60	60

Ratio: 5.533  
Gaps: 0  
Percent Similarity: 100.000  
Percent Identity: 100.000

```
alignment_block:
  "00-500-011-2" x 11725534
  "00-500-011-2" x 11725534
```

Align seg 1/1 to: AAZ25534 from: 1 to: 180

25 AlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAshSerAlaGlyIY 41  
1 GCACCTG

**1**

1

on the development of drugs acting on galanin binding, such as function improvers, appetite improvers, and function regulators. mb, kidney, prostate, testis or skeletal muscle. AAY45129



100

womb, kidney, prostate, testis or sk

The present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGGG or one substantially identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin binding, such as memory function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. AAY45129 to AAY45154

CC and AAZ25518 to AAZ25552 represent sequences used in the exemplification  
CC of the present invention.

XX  
SQ  
Sequence 1007 BP; 256 A; 293 C; 244 G; 214 T; 0 other;

alignment_scores:		
Quality:	323.00	Length: 140
Ratio:	3.106	Gaps: 5
Percent Similarity:	74.286	Percent Identity: 57.857

alignment\_block: US-09-689-911-2 x AAZ25531

Align seq 1/1 to: AAZ25531 from: 1 to: 1007

84 ACTGTCCTCTGATCGTTCTTGCAGTC...CTGCTCAGCCTGATGGAGTC 130  
 21 rProlaSerAlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnS 38  
 131 TCCAGCCTCTGCTCGGTCCACAGGGGGCAGGAGGCTGACGCCCTCAACA 180  
 38 eAlaGlyTyrLeuLeuGlyProValLeuHisIstLeuProGlnMetGlyAsp 54  
 181 GTGCTGGTTACCTCTGGGTCCCGCTACTCATCTCGGCCTCCAGGCTGAA 230

55 GlnAspGlyLysArgGluThrAlaLeuCluIleLeuAspleuTtpLysAl 71  
||||| ::||| ||||| ||||| |||||  
231 GGAGCGGAAGGGGAAGACAGCCTCGGATCTCGACTGTGGAAGC 280

71 a l e A s p G l y L e u P r o T y r S e r H i s P r o G l n P r o S e r L y s A r g A s n V   88  
|||||  
281 C A T T C A T G G C G C C C C A T C C C C A G T C C A G T T G G C C T C C A A G A R G A G T C   330

88 alMetGluThrPheAlaLysProGluIleGGlyClylysAlaArgDys.Hi 104  
:: |||||  
331 TCGG GAGACTTCGCACCACTGTGA.....GTACA 367

104 sArgArgGluThrProThr.GlyGluGlyGluGlnGlySerGlyArgGln 120  
120  
168  
368

121 ...SerLeuGluAspLeuGlyMetIeuSerMetLysIleProLysGluGlu 136  
119 mACGACCGCTTACATCTACGACAGCTCTCCAGCAACCTTCAAGAGCAAA 467

```

136 uAspValLeuLysSer 141
      :||::|||::|||
150 NCACCCCCCC(C)CC(C)C 193

```

seq name: /SDS1/acadata/geneseq/geneseq/NA1999.DAT:AAZ25533

```
seq_documentation_block:
ID      AA225533 standard; cDNA; 180 BP.
```

XX  
AC AAZ25533;

21-DEC-1999 (first entry)

Receptor binding peptide encoding cDNA SEQ ID NO:39.

Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss.

XX Rattus sp.

AA PN WO9948920-A1.

30-SEP-1999.

XX	24-MAR-1999;	99WO-JP01482.
PF		
XX	25-MAR-1998;	98JP-0078139.
PR	21-SEP-1998;	98JP-0266972.
PR		
XX	(TAKE ) TAKEDA CHEM IND LTD.	
PA		

XX Ohtaki T, Matsui H, Ishibashi Y, Ogi K, Kitada C;  
PI  
XX wpt: 1999-572170/48.  
DE

XX Peptides binding to galanin receptor proteins, used to, e.g. improve  
PT kidney functioning -

xx  
ps  
Claim 11: page 142; 153pp; Japanese.

xx The present invention describes peptides (I) binding to galanin receptor  
CC proteins. (I) contain the sequence APAHRGRGG or one substantially  
CC identical to it, and their precursors, salts, amides and esters, which  
CC bind especially to rat galanin receptor proteins. Products from the  
CC present invention are used in assays of galanin/galanin receptor binding  
CC and the development of drugs acting on galanin binding, such as memory  
CC function improvers, appetite improvers, and function regulators for the  
CC womb, kidney, prostate, testis or skeletal muscle. AA45129 to AA45134  
CC and AA225518 to AA225552 represent sequences used in the exemplification  
CC of the present invention.

Sequence 180 BP; 39 A; 57 C; 47 G; 37 T; 0 other;

alignment_scores:		
Quality:	243.00	Length: 58
Ratio:	4.673	Gaps: 0
Percent Similarity:	89.655	Percent Identity: 77.586

```
alignment_block: US-09-689-911-2 x AAZ25533
```

Align seq 1/1 to: AAZ25533 from: 1 to: 180

25 AlaProAlaHisArgGlyArgGlyGlyTyrThrLeuAsnSerAlaGlyTy 41  
|||||  
1 GCACCTGCTCACAGGGGACGAGGAGGCTGGACCCCTCAATAGTCTGGTTA 50

41 rLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGlyL 58  
|||||  
51 CCTCCTGGGTCTGTCTCCACCTTTCCTCAAGGCCCAACACGGGCAGGA 100  
|||||

58 ysArgGluThrAlaLeuGluIleLeuAspLeuTrpLysAlaIleAspGly 74  
|| : : : : :  
101 AGACAGACTCAGCTCTTGAGATCCTAGACCTGTGAAGGCCATGATGGG 150

```

75 LeuProTyrSerHisProProGln 82
   |||||
151 CTCCCTTATTCCCGCTCTCCAAGG 174

```

seq\_name: /SIDS1/qcdata/geneseq/geneseq/NA2001.DAT:AAF44070

seq\_documentation\_block:

XX  
RAF 44070  
RAF 44070

XX  
DT  
23-MAR-200

XX DNA encoding a rat physiological

XX physiologically active protein; galanin receptor; G

KW fibroblast growth factor; us.  
XX

XX  
Raculus sp.

PN JP2000270871-A.  
 XX 03-OCT-2000.  
 XX 24-MAR-1999; 99JJP-0080303.  
 XX 24-MAR-1999; 99JJP-0080303.  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 XX WPI; 2001-019315/03.  
 XX  
 XX Preparation of a new physiologically active peptide having a cleaved  
 PT cysteine residue as N-terminal -  
 XX  
 XX Disclosure; Page 35-36; 44pp; Japanese.  
 XX  
 XX This invention relates to a method for the preparation of a  
 CC physiologically active peptide having a cleaved cysteine residue at the  
 CC end N-terminal, and has any of the amino acid sequences given in  
 CC AAB65131 - AAB65136. The invention includes sequences AAB65137 - AAB65153  
 CC which represent proteins related to the main proteins of the invention,  
 CC including galanin receptors, and basic fibroblast growth factor. DNA  
 CC sequences AAF44065 - AAF44071 and PCR primers AAF44072 - AAF44086 are  
 CC used in the isolation and characterisation of DNA encoding the proteins  
 CC of the invention.  
 XX  
 XX Sequence 180 BP; 39 A; 57 C; 47 G; 37 T; 0 other;

alignment\_scores:  
 Quality: 243.00 Length: 58  
 Ratio: 4.673 Gaps: 0  
 Percent Similarity: 89.655 Percent Identity: 77.586  
 alignment\_block:  
 US-09-689-911-2 x AAF44070 ..  
 Align seg 1/1 to: AAF44070 from: 1 to: 180  
 25 AlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerAlaGlyTy 41  
 1 GCACCTGCTCACAGGGGACGAGGAGGCTGGACCCCTCAATAGTGTGTTA 50  
 41 rLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGlyL 58  
 51 CCTCTGGTCTGTCCTCCACCTTCTCTCAAGGCCAACACGAGGCGAGGA 100  
 58 ysArgGluThrAlaLeuGluLeuLeuAspLeuTrpLysAlaIleAspGly 74  
 101 AGACAGACTCAGCTCTGAGATCTAGACCTGTGGAGGCCATAGATGGG 150  
 75 LeuProTyrSerHisProGln 82  
 151 CTCCTTTATTCCCGCTCTCCAAGG 174

seq\_name: /SIDSI/gcgdata/geneseq/geneseq/NA2001.DAT:AAF44067  
 seq\_documentation\_block:  
 ID AAF44067 standard; DNA; 567 BP.  
 XX AAF44067;  
 AC  
 XX 23-MAR-2001 (first entry)  
 DT  
 XX bFGF (human fibroblast growth factor) DNA sequence SEQ ID 17.  
 DE  
 XX Physiologically active protein; galanin receptor; GALR; FGF;  
 KW fibroblast growth factor; ds.  
 XX  
 OS Homo sapiens.  
 XX JP2000270871-A.  
 PN

XX 03-OCT-2000.  
 XX 24-MAR-1999; 99JJP-0080303.  
 XX 24-MAR-1999; 99JJP-0080303.  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 XX WPI; 2001-019315/03.  
 XX  
 XX Preparation of a new physiologically active peptide having a cleaved  
 PT cysteine residue as N-terminal -  
 XX  
 XX Disclosure; Page 7; 44pp; Japanese.  
 XX  
 XX This invention relates to a method for the preparation of a  
 CC physiologically active peptide having a cleaved cysteine residue at the  
 CC end N-terminal, and has any of the amino acid sequences given in  
 CC AAB65131 - AAB65136. The invention includes sequences AAB65137 - AAB65153  
 CC which represent proteins related to the main proteins of the invention,  
 CC including galanin receptors, and basic fibroblast growth factor. DNA  
 CC sequences AAF44065 - AAF44071 and PCR primers AAF44072 - AAF44086 are  
 CC used in the isolation and characterisation of DNA encoding the proteins  
 CC of the invention.  
 XX  
 XX Sequence 567 BP; 133 A; 154 C; 163 G; 117 T; 0 other;

alignment\_scores:  
 Quality: 232.00 Length: 75  
 Ratio: 4.070 Gaps: 2  
 Percent Similarity: 76.000 Percent Identity: 65.333  
 alignment\_block:  
 US-09-689-911-2 x AAF44067 ..  
 Align seg 1/1 to: AAF44067 from: 1 to: 567  
 25 AlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerAlaGlyTy 41  
 1 GCTCCGGTCCACAGGGGCGAGAGGCTGGACCCCTCAACAGTGTGTTA 50  
 41 rLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGlyL 58  
 51 CCTCTGGTCTGTCCTCCACCTTCTCTCAAGGCCAACACGAGGCGGGA 100  
 58 ysArgGluThrAlaLeuGluLeuLeuAspLeuTrpLysAlaIleAspGly 74  
 101 AGGGGAAGACAGCCCTCGGACATCTGGACCTGTGGAGGCCATGATGGG 150  
 75 LeuProTyrSerHisProGlnProSerLysArgAsnValMetGluTh 91  
 151 CTCCTCTAT.....CCCCAG.....TCTCAGTTGGCTCCTG 182  
 91 rPheAlaLysProGluLeuGlyGly 99  
 183 CCCAGCATTCGCCGAGGATGGCGGC 207

seq\_name: /SIDSI/gcgdata/geneseq/geneseq/NA2001.DAT:AAF44068  
 seq\_documentation\_block:  
 ID AAF44068 standard; DNA; 567 BP.  
 XX AAF44068;  
 AC  
 XX 23-MAR-2001 (first entry)  
 DT  
 XX bFGF (human fibroblast growth factor) DNA sequence SEQ ID 18.  
 DE  
 XX Physiologically active protein; galanin receptor; GALR; FGF;  
 KW fibroblast growth factor; ds.  
 XX



```
seq_name: /SDS1/gcdata/geneseq/NA2001.DAT:AAF44069
seq_documentation_block:
ID   AAF44069 standard; DNA; 180 BP.
XX
```

```
seq_name: /SID1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ25532
seq_documentation_block:
ID   AAZ25532 standard; cDNA; 180 BP.
XX
XX   AAZ25532;
XX
XX   21-DEC-1999 (first entry)
XX
XX   Porcine ligand (1-60) encoding cDNA.
XX
```

•  
•  
•  
•

OM of: US-09-689-911-2 to: GenEmbl.\* out\_format : pfs

Date: Mar 3, 2002 12:47 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=frame+p2n.model -DEV=slp  
-O=/cgn2\_1/USPTO\_spool/US09689911/runat\_02032002\_201655\_18764/app\_query.fasta\_1.199  
-DB=GenEmbl -QEMT=fastcap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000  
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500  
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000  
-DEPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000  
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZ=500  
-MINLEN=0 -WAXLEN=200000000 -USER=US09689911@cgnl\_1.4572  
-NCPU=6 -ICPU=3 -LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30  
-NO\_XLUPY -WAIT -THREADS=1

Search information block:

Query: US-09-689-911-2

Query length: 141

Database: GenEmbl.\*

Database sequences: 1472140

Database length: -341344837

Search time (sec): 1464.440000

score\_list:

Sequence	Strd Orig	ZScore	Escore	Len	Documentation
gb_pat:AX112343	+	734.00	1101.51	456-53	AX112343 Sequence 1 from Patent
gb_pat:AX112345	+	580.50	873.13	2.3e-40	AX112345 Sequence 3 from Patent
gb_pr:AF188492	+	580.50	866.47	5.5e-40	AF188492 Homo sapiens clone pgr
gb_pr:AF188493	+	580.50	866.47	5.5e-40	AF188493 Homo sapiens clone pgr
gb_to:AF188491	+	348.50	521.42	9.1e-21	AF188491 Rattus norvegicus gale
gb_to:AF188491	+	348.50	521.42	9.1e-21	AF188491 Rattus norvegicus gale
gb_om:AF188490	+	342.00	509.42	4.2e-20	AF188490 Sus scrofa galanin-like
gb_pr:AC011506	+	280.00	385.56	3.4e-13	AC011506 Homo sapiens chrom
gb_pr:AC011506	+	280.00	385.56	3.4e-13	AC011506 Homo sapiens chrom
gb_hg:AC024580	-	148.00	183.39	0.0614	AC024580 Homo sapiens chrom
gb_hg:AC024580	-	148.00	183.39	0.0614	AC024580 Homo sapiens chrom
gb_to:RATGALA	+	104.50	156.46	1.94	M18102 Rat galanin mRNA, comple
gb_to:RATGALA	+	104.50	156.46	1.94	M18102 Rat galanin mRNA, comple
gb_to:RATGALA	+	101.50	121.25	177.64	J03624 Rat galanin (a neuropept
gb_hg:AC087454	+	101.50	121.25	177.64	AC087454 Homo sapiens chrom
gb_hg:AC073548	+	99.50	150.10	4.39	AC073548 Homo sapiens chrom
gb_hg:AC073548	+	99.50	150.10	4.39	AC073548 Homo sapiens chrom
gb_pat:AF8025	+	99.50	150.10	4.39	AF8025 Human preprogalanin cDNA
gb_ov:AP003795	+	99.00	110.53	701.74	AP003795 Gallus gallus genom
gb_to:AF272146	+	98.50	141.20	13.74	AF272146 Mus musculus transmem
gb_to:AF272146	+	98.50	141.20	13.74	AF272146 Mus musculus transmem
gb_hg:AC011571	-	97.50	109.68	783.42	AC011571 Homo sapiens clone
gb_hg:AC011571	-	97.50	109.68	783.42	AC011571 Homo sapiens clone
gb_om:BTGALAN	+	96.50	145.29	8.14	X12582 Bovine preprogalanin mRN
gb_hg:AL445199	-	96.50	145.29	8.14	AL445199 Homo sapiens chrom
gb_om:AP003199	-	96.00	107.89	985.50	AP003199 Oryza sativa genom
gb_hg:AC073396	-	96.00	106.71	1.1e+03	AC073396 Homo sapiens chrom
gb_hg:AC073396	-	96.00	106.71	1.1e+03	AC073396 Homo sapiens chrom
gb_hg:AC073732	+	95.50	105.38	1.4e+03	AC073732 Mus musculus clone
gb_hg:AC073732	+	95.50	105.38	1.4e+03	AC073732 Mus musculus clone
gb_pr:AC013272	-	95.00	104.54	1.5e+03	AC013272 Homo sapiens chrom
gb_hg:AC013272	-	95.00	104.54	1.5e+03	AC013272 Homo sapiens chrom
gb_ov:AF141935	+	94.50	114.02	448.96	AF141935 Coturnix coturnix jap
gb_ov:AF141935	+	94.50	114.02	448.96	AF141935 Coturnix coturnix jap
gb_pr:AB012723	+	94.50	103.15	1.8e+03	AB012723 Homo sapiens gene fo
gb_hg:AC024514	-	94.50	103.15	1.8e+03	AC024514 Homo sapiens chrom
gb_hg:AL589733	+	94.50	103.21	17.74	AL589733 Homo sapiens chrom
gb_ov:AF141936	+	94.00	103.50	1.7e+03	AF141936 Coturnix coturnix jap
gb_ov:AF141936	+	94.00	103.50	1.7e+03	AF141936 Coturnix coturnix jap
gb_pl:AF021633	+	93.50	130.94	51.26	AF021633 Oryza sativa genom
gb_hg:AF276756	+	93.50	103.79	1.7e+03	AF276756 Homo sapiens chrom
gb_hg:AC021500	+	93.50	103.08	1.6e+03	AC021500 Homo sapiens chrom
gb_hg:AC021500	+	93.50	103.08	1.6e+03	AC021500 Homo sapiens chrom
gb_hg:AC019122	-	93.50	101.61	2.2e+03	AC019122 Homo sapiens chrom
gb_hg:AC019122	-	93.50	101.61	2.2e+03	AC019122 Homo sapiens chrom
gb_hg:AC011333	+	93.00	102.68	1.9e+03	AC011333 Homo sapiens chrom
gb_hg:AC011333	+	93.00	102.68	1.9e+03	AC011333 Homo sapiens chrom
gb_to:AC069014	+	93.00	101.76	2.2e+03	AC069014 Mus musculus 11 BAC
gb_hg:AL591425	+	93.00	101.75	2.2e+03	AL591425 Mus musculus chrom
gb_hg:AC026408	-	93.00	101.11	2.4e+03	AC026408 Homo sapiens chrom

gb\_hgt:AC068525 + 92.50 107.26 1.1e+03 71631 ! AC068525 Homo sapiens chr  
gb\_pr:AC018712 + 92.50 102.00 2.1e+03 156833 ! AC018712 Homo sapiens B  
gb\_hgt:AC020681 + 92.50 101.07 2.4e+03 180192 ! AC020681 Homo sapiens C  
gb\_hgt:AC087898 + 92.50 100.51 2.5e+03 195630 ! AC087898 Mus musculus c  
gb\_hgt:AC074027 + 92.50 100.39 2.6e+03 199359 ! AC074027 Mus musculus c  
seq\_name: gb\_pat:AX112343  
seq\_documentation\_block: 426 bp DNA PAT 01-MAY-2001  
LOCUS AX112343  
DEFINITION Sequence 1 from Patent WO0127273.  
ACCESSION AX112343  
VERSION AX112343.1 GI:13939104  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 426)  
AUTHORS Turner,C.A., Donoho,G., Wang,X., Hilbun,E., Zambrowicz,B. and  
Sands,A.T.  
TITLE Human galanin family proteins and polynucleotides encoding the same  
JOURNAL Patent: WO 0127273-A 1 19-APR-2001;  
Lexicon Genetics Incorporated (US)  
FEATURES  
Location/Qualifiers  
Source  
1..426  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 107 a 127 c 120 g 72 t  
ORIGIN

alignment\_scores:  
Quality: 734.00 Length: 141  
Ratio: 5.206 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000  
alignment\_block:  
US-09-689-911-2 x AX112343 ..  
Align seg 1/1 to: AX112343 from: 1 to: 426  
1 MetAlaProSerValProLeuValLeuLeuValLeuLeuLeuSe 17  
|||||  
1 ATGGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 50  
|||||  
17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyGly 34  
|||||  
51 CTGGCGAGAGACCTCCAGACCTCCAGACCTCCAGACCTCCAG 100  
|||||  
34 rPthrLeuAsnSerAlaGlyTyrLeuLeuGlyProValLeu 50  
|||||  
101 GGACCTCAATAGTGTGGTACCTTCTGGTCCCTCCCTCCCT 150  
|||||  
51 GlnMetGlyAspGlnaspGlyLysArgGluThrAlaLeuGlu 67  
|||||  
151 CAAATGGTGACCAAGACGGAAGAGAGAGAGAGAGAGAGAG 200  
|||||  
67 pLeuThrLysAlaIleAspGlyLeuProTyrSerHisProG 84  
|||||  
201 CCTGTGAAGAGCCATCGATGGGTCCCTCCCTCCCTCCCT 250  
|||||  
84 erLysArgAsnValMetGluThrPheAlaLysProGluLeu 100  
|||||  
251 CCAAGAGGAATGTGGAGACGCTTTCCTCCCAACAGAGATT 300  
|||||  
101 AlaArgLysHisArgArgGluThrProThrGlyGluGlySe 117  
|||||  
301 GCCAGGAAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 350  
|||||  
117 rGlyArgGlnSerLeuGluAspLeuGlyMetLeuSerMetL 134  
|||||  
351 TGGCAGGAGAGCTTAGAGGATCTGGGATCTGGGATCTGGG 400  
|||||

255 .....GATCTGGGCACTGCTCAAGCAAGAAAAATCCCA 323

233 CAAATGGGTGACCAAC

[illegible]

```

ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 947)
Ohtaki,T., Kumano,S., Ishibashi,Y., Ogi,K., Matsui,H., Harada,M.,
Kitada,C., Kurokawa,T., Onda,H. and Fujino,M.
Isolation and cDNA cloning of a novel galanin-like peptide (GALP)
from porcine hypothalamus
J. Biol. Chem. 274 (52), 37041-37045 (1999)
20069685
REFERENCE 2 (bases 1 to 947)
AUTHORS Ohtaki,T. and Kumano,S.
Direct Submission
Submitted (21-SEP-1999) Discovery Res. Labs. 1, Takeda Chemical
Industries, Ltd., Wadai 10, Tsukuba, Ibaraki 300-4293, Japan
Location/Qualifiers
1..947
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="pGR2HL02"
83..433
/note="neuropeptide"
/codon_start=1
/product="galanin-like peptide precursor"
/protein_id="AAF19725.1"
/db_xref="GI:6634716"
/translation="MAPPSVPVLVLLVLLSLAETPASAPAHRGKGVTLNSAGYLLG
PVLHLPQMGDQDKRTALEILDWKADIGLPSYHPQPSKRVMTFAKPEIGDLGM
LSMKIPKEEDVLKS"
BASE COUNT 246 a 212 g 248 t
ORIGIN
alignment_scores:
Quality: 580.50 Length: 141
Ratio: 5.004 Gaps: 1
Percent Similarity: 82.270 Percent Identity: 82.270
alignment_block:
US-09-689-911-2 x AF188493 ..
Align seq 1/1 to: AF188493 from: 1 to: 947

```

VHLSSKANOGKRTDSDALEILDLMKALDGLPYSRSPRMTKRSMTGETVKPRGDLRIY  
DKNVPDEATLNL"

BASE COUNT 195 a 201 c 143 g 155 t

ORIGIN

# alignment\_scores:

Quality: 348.50 Length: 132  
Ratio: 3.747 Gaps: 1  
Percent Similarity: 70.455 Percent Identity: 54.545

# alignment\_block:

US-09-689-911-2 x AF188491 ..

Align seg 1/1 to: AF188491 from: 1 to: 694

```

8 LeuValLeuLeuValLeuLeuSerLeuLeuAlaGluThrProAlaSe 24
|||||.....|.....|.....|.....|.....|.....|
144 CTGTCCTCTTCTCACCACCTCTGTAAGCCTCGCAGAAACACCACTC 193
24 rAlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerAlaGlyT 41
|||||.....|.....|.....|.....|.....|.....|
194 TGCACCTGCTCACAGGGACGAGGAGGCTGGACCCTCAATAGTCTGTT 243
41 yrLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGly 57
|||||.....|.....|.....|.....|.....|.....|
244 ACCTCTGGGTCCTGCTCCACCTTCTCCTCAAGGCCAACCAAGGCGAGG 293
58 LysArgGluThrAlaLeuGluLeuLeuAspLeuTrpLysAlaIleAspG1 74
|||||.....|.....|.....|.....|.....|.....|
294 AAGACAGACTCAGCTCTTGAGATCTAGACCTGTGGAAGGCATAGATGG 343
74 yLeuProTyTyrSerHisProGlnProSerLysArgAsnValMetGluT 91
|||||.....|.....|.....|.....|.....|.....|
344 GCTCCCTATTCCGCTCTCAAGGATGACCAAAAGGTCAATGGGAGAAA 393
91 hrPheAlaLysProGluLeuGlyGlyLysAlaArgLysHisArgArgL 107
|||||.....|.....|.....|.....|.....|.....|
394 CGTTGTCAAGCGAGGACTGGA.....|.....|.....|.....| 416
108 ThrProThrGlyGluGlyGluGlnGlySerGlyArgGlnSerLeuGluAs 124
|||||.....|.....|.....|.....|.....|.....|
417 .....|.....|.....|.....|.....|.....|.....| 418
124 pLeuGlyMetLeuSerMetLysLeuProLysGluGluAspValLeu 139
|||||.....|.....|.....|.....|.....|.....|
419 TCTGCGCATAGTGCACAAAGAATGTTCCGGATGAAGACCCACCTG 464

```

seq\_name: gb\_on:AF188490

# seq\_documentation\_block:

LOCUS AF188490 974 bp mRNA MAM 24-DEC-1999  
DEFINITION Sus scrofa galanin-like peptide precursor, mRNA, complete cds.  
ACCESSION AF188490  
VERSION AF188490.1 GI:6634709  
KEYWORDS  
SOURCE pig.

# ORGANISM

Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

# REFERENCE

1 (bases 1 to 974)  
Ohtaki, T., Kumano, S., Ishibashi, Y., Ogi, K., Matsui, H., Harada, M.,  
Kitada, C., Kurokawa, T., Onda, H. and Fujino, M.  
Isolation and cDNA cloning of a novel galanin-like peptide (GALP)  
from porcine hypothalamus  
J. Biol. Chem. 274 (52), 37041-37045 (1999)

# JOURNAL

MEDLINE 20069685

# REFERENCE

2 (bases 1 to 974)  
Ohtaki, T. and Kumano, S.  
Direct Submission  
Submitted (21-SEP-1999) Discovery Res. Labs. 1, Takeda Chemical  
Industries, Ltd., Wadai 10, Tsukuba, Ibaraki 300-4293, Japan

# JOURNAL

TITLE

FEATURES

# source

1. .974  
/organism="Sus scrofa"  
/db\_xref="taxon:9823"  
35\_397

# CDS

/note="neuropeptide"  
/codon\_start=1  
/product="galanin-like peptide precursor"  
/protein\_id="AA19722.1"  
/db\_xref="GI:6634710"  
/translation="MALTVPLIVLAVLLSLMESPASAPVHRGCGWTLSAGYLLGPV  
LHPPSRAEGGKGKTAIGLIDLMKALDGLPYSQSLAKRSLSGETFAKPDGSGVTFVGV  
PDVVPKRIKRPRTTRFOI"  
BASE COUNT 258 a 278 c 229 g 209 t  
ORIGIN

# alignment\_scores:

Quality: 342.00 Length: 140  
Ratio: 3.320 Gaps: 5  
Percent Similarity: 73.571 Percent Identity: 57.857

# alignment\_block:

US-09-689-911-2 x AF188490 ..

Align seg 1/1 to: AF188490 from: 1 to: 974

```

5 SerValProLeuValLeuLeuValLeuLeuSerLeuLeuAlaGluTh 21
|||||.....|.....|.....|.....|.....|.....|
44 ACTGTCCTCTGATCGTCTTTCAGATC...CTGCTCAGCCTGATGGAGTC 90
21 rProAlaSerAlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnS 38
|||||.....|.....|.....|.....|.....|.....|
91 TCCAGCCTCTGCTCCGTCGTCACAGGGCGGAGGAGGCTGGACCTCAACA 140
38 exAlaGlyTyrLeuLeuGlyProValLeuHisLeuProGlnMetGlyAsp 54
|||||.....|.....|.....|.....|.....|.....|
141 GTGCTGTTTACCTCTCGGTGCTCCGTACTCCATCCGCTCCAGGCTGAA 190
55 GlnAspGlyLysArgGluThrAlaLeuGluLeuLeuAspLeuTrpLysAl 71
|||||.....|.....|.....|.....|.....|.....|
191 GGAGCGGGAGGGGAGAGACAGCCCTCGGATCTCTGGACCTTGGAAAGGC 240
71 alLeuAspGlyLeuProTyTyrSerHisProGlnProSerLysArgAsnV 88
|||||.....|.....|.....|.....|.....|.....|
241 CATTGATGGCTCCCTCATCCAGCTCTCAGTTGGCTCTCCAGAGGAGTC 290
88 alMetGluThrPheAlaLysProGluLeuGlyGlyLysAlaArgLys.Hi 104
|||||.....|.....|.....|.....|.....|.....|
291 TGGGGAGACTTTCGCCAAACACAGACTCTGGA.....|.....|.....| 328
104 sArgArgGluThrProThr.GlyGluGlyGluGlnGlySerGlyArgGln 120
|||||.....|.....|.....|.....|.....|.....|
329 TTTGTTGGAGTTCCTGACGTGTCGCGTGGAAACGAATCCGACCAAGAAC 378
121 ...SerLeuGluAspLeuGlyMetLeuSerMetLysIleProLysGluGl 136
|||||.....|.....|.....|.....|.....|.....|
379 TACGAGGTTTCAGATCTAGGCAAGCTCTGCAAGAACAGTTCCCAAGAGGAA 428
136 uAspValLeuLysSer 141
|||||.....|.....|.....|.....|.....|.....|
429 AGATGCTTGGCGTCA 444

```

seq\_name: gb\_pr:AC011506

# seq\_documentation\_block:

LOCUS AC011506 100110 bp DNA PRI 21-APR-2000  
DEFINITION Homo sapiens chromosome 19 clone CTD-2086L14, complete sequence.  
ACCESSION AC011506  
VERSION AC011506.3 GI:7630361  
KEYWORDS HTG.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mon Mar '4 11:27:01 2002

```

REFERENCE
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1 (bases 1 to 100110)
JOURNAL      DOE Joint Genome Institute and Stanford Human Genome Center.
REFERENCE    Direct Submission
AUTHORS      Unpublished
TITLE        2 (bases 1 to 100110)
JOURNAL      DOE Joint Genome Institute.
REFERENCE    Direct Submission
AUTHORS      DOE Joint Genome Institute.
TITLE        Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint
JOURNAL      Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE    3 (bases 1 to 100110)
AUTHORS      DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE        Direct Submission
JOURNAL      Submitted (21-APR-2000) DOE Joint Genome Institute, 2800 Mitchell
COMMENT      Drive, Walnut Creek, CA 94598, USA
              On Apr 21, 2000 this sequence version replaced gi:6910529.
              Draft Sequence Produced by DOE Joint Genome Institute
              www.jgi.doe.gov
              Finishing Completed at Stanford Human Genome Center
              www.shgc.stanford.edu
              Quality: Phrap Quality >=40 99.9% of Sequence;
              Estimated Total Number of Errors is 0.2.
              STS Content:
              WI-11903 G21646.
              Location/Qualifiers
                source          1..100110
                organism="Homo sapiens"
                db_xref="taxon:9606"
                chromosome="19"
                clone="CTD-2086L14"
              BASE COUNT      26449 a 23149 c 22857 g 27655 t
              ORIGIN
alignment_scores:
  Quality: 280.00      Length: 55
  Ratio: 5.283        Gaps: 0
  Percent Similarity: 96.364      Percent Identity: 94.545
alignment_block:
  US-09-689-911-2 x AC011506 ..
Align seg 1/1 to: AC011506 from: 1 to: 100110
72 1leAspGlyLeuProTyrSerHisProGlnProSerLysArgAsnVa 88
  ::::::::::::::::::::::::::::::::::::::::::::::::::
734 CTAGACGGGCTCCCTCTACTCCACCTCCACAGCCCTCCAGAGGAATGT 783
  ::::::::::::::::::::::::::::::::::::::::::::::::::
88 1MetGluThrPheAlaLysProGluIleGlyLysAlaArgLysHisa 105
  ::::::::::::::::::::::::::::::::::::::::::::::::::
784 GATGAGACGTTTGCCAAACACAGAGATTGGAGTTAAGCCAGGAACACA 833
  ::::::::::::::::::::::::::::::::::::::::::::::::::
105 rgArgGluThrProThrGlyGluGlyGluGlnGlnGlySerGlyArgGlnSer 121
  ::::::::::::::::::::::::::::::::::::::::::::::::::
834 GAAGAGACACCGACGAGAGAGGGGGAACAGGAAGTGGCAGGACAGC 883
  ::::::::::::::::::::::::::::::::::::::::::::::::::
122 LeuGluAspLeuGly 126
  ::::::::::::::
884 TTAGAGGGTAAGGA 898
  ::::::::::::::
seq_name: gb_htg:AC023887
seq_documentation_block:
LOCUS      AC023887 164824 bp DNA HTG 17-AUG-2000
DEFINITION Homo sapiens chromosome 19 clone RP11-541M19, WORKING DRAFT
SEQUENCE   SEQUENCE, 8 unordered pieces.
ACCESSION  AC023887
VERSION    AC023887.4 GI:9838262
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Waterston,R.H.
TITLE        The sequence of Homo sapiens clone
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 164824)
AUTHORS      Waterston,R.H.
TITLE        Direct Submission
JOURNAL      Submitted (18-FEB-2000) Genome Sequencing Center, Washington
COMMENT      University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
              On Aug 17, 2000 this sequence version replaced gi:7631054.
              -----
              Center: Washington University Genome Sequencing Center
              Center code: WUGSC
              Web site: http://genome.wustl.edu/gsc/index.shtml
              -----
              Project Information
              Center project name: H.NH0541M19
              -----
              Summary Statistics
              Sequencing vector: M13; 82%
              Chemistry: Dye-terminator Big Dye; 18% of reads
              Assembly program: Phrap; version 0.990319
              Consensus quality: 160238 bases at least Q40
              Consensus quality: 161837 bases at least Q30
              Consensus quality: 162813 bases at least Q20
              Insert size: 170000; agarose-fp
              Insert size: 165317; sum-of-contigs
              Quality coverage: 6.34 in Q20 bases; agarose-fp
              Quality coverage: 6.53 in Q20 bases; sum-of-contigs
              -----
              * NOTE: This is a 'working draft' sequence. It currently
              * consists of 8 contigs. The true order of the pieces
              * is not known and their order in this sequence record is
              * arbitrary. Gaps between the contigs are represented as
              * runs of N, but the exact sizes of the gaps are unknown.
              * This record will be updated with the finished sequence
              * as soon as it is available and the accession number will
              * be preserved.
              *
              1
              2092: contig of 2092 bp in length
              2192: gap of unknown length
              7044: contig of 4852 bp in length
              7144: gap of unknown length
              19499: contig of 12355 bp in length
              19599: gap of unknown length
              34475: contig of 14876 bp in length
              34575: gap of unknown length
              47285: contig of 12710 bp in length
              47385: gap of unknown length
              47386: contig of 24885 bp in length
              72271: gap of unknown length
              72371: contig of 24851 bp in length
              97321: gap of unknown length
              97322 164824: contig of 67503 bp in length.
              -----
              Location/Qualifiers
                source          1..164824
                organism="Homo sapiens"
                db_xref="taxon:9606"
                chromosome="19"
                clone="RP11-541M19"
              misc_feature
                1..2092
                  note="assembly_name:Contig9
                  vector_end:T7
                  vector_side:right"
                2193..7044
                  note="assembly_name:Contig10"
                7145..19499
                  note="assembly_name:Contig11"
                19600..34475
                  note="assembly_name:Contig12"
                34576..47285
                  note="assembly_name:Contig13"

```

```

misc_feature      47386..72270
                  /note="assembly_name:Contig14"
misc_feature      72371..97221
                  /note="assembly_name:Contig15
clone_end:SP6
vector_side:right"
misc_feature      97322..164824
                  /note="assembly_name:Contig16"
BASE COUNT      38305 a 41699 c 42797 g 41321 t 702 others
ORIGIN

```

```

alignment_scores:
  Quality: 280.00      Length: 55
  Ratio: 5.283         Gaps: 0
  Percent Similarity: 96.364  Percent Identity: 94.545
alignment_block:
  US-09-689-911-2 x AC023887 ..

```

Align seg 1/1 to: AC023887 from: 1 to: 164824

```

77  ILeAspGlyLeuProTyrSerHisProGlnProSerLysArgAsnVa 88
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
87745  CTAGATGGCTCCCTACTCTCCACCCCTCCACAGCCCTCCACAGAGGAATGT 87794
      |
88  lMetGluThrPheAlaLysProGluIleGlyGlyLysAlaArgLysHisA 105
      |::::::::::::::::::::::::::::::::::::::::::::::::::::
87795  GATGCACACGTTTCCCAACACAGAGATTGGAGSTAAAGCCAGGAACACA 87844
      |
105  rArgGluThrProThrGlyGluGlyGluGlnGlySerGlyArgGlnSer 121
      |::::::::::::::::::::::::::::::::::::::::::::::::::::
87845  GAAGAGAGACACCGACAGGAGGAGGGGGAACAGAGAGTGCAGGCAGGC 87894
      |
122  LeuGluAspLeuGly 126
      |::::|
87895  TTAGAGGGTAAAGGA 87909

```

seq\_name: gb\_htg:AC024580

```

seq_documentation_block:
  LOCUS      AC024580      200603 bp      DNA      HTG      20-APR-2001
  DEFINITION Homo sapiens chromosome 19 clone CTD-2621117, WORKING DRAFT
  SEQUENCE: 51 unordered pieces.
  ACCESSION      AC024580
  VERSION      AC024580.4  GI:13699641
  KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
  SOURCE      human.
  ORGANISM      Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE      1 (bases 1 to 200603)
                  DOE Joint Genome Institute.
                  Sequencing of Human Chromosome 19
                  Unpublished
  REFERENCE      2 (bases 1 to 200603)
                  DOE Joint Genome Institute.
                  Direct Submission
                  Title
                  Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint
                  Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                  On Apr 20, 2001 this sequence version replaced gi:9954666.
                  -----Genome Center
                  Center: Joint Genome Institute
                  Center Code: JGI
                  Web site: http://www.jgi.doe.gov
                  -----
                  Project Information
                  Center Project Name: 836654, BC801678
                  Center clone name: CITB-E1_2621117
                  -----
                  Summary Statistics
                  Consensus quality: 157877 bases at least Q40
                  Consensus quality: 174287 bases at least Q30

```

Consensus quality: 180284 bases at least Q20  
 Estimated insert size: 192390; agarose-fp estimation  
 Estimated insert size: 195603; sum-of-contigs estimation  
 Quality coverage: 5.09 in Q20 bases; agarose-fp estimation  
 Quality coverage: 5.01 in Q20 bases; sum-of-contigs estimation.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 51 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

```

      1 1144: contig of 1144 bp in length
      * 1145: gap of unknown length
      * 1245: contig of 1772 bp in length
      * 3016: gap of unknown length
      * 3116: gap of unknown length
      * 3117: contig of 1110 bp in length
      * 4226: gap of unknown length
      * 4326: gap of unknown length
      * 4327: contig of 1124 bp in length
      * 5451: gap of unknown length
      * 5550: contig of 1063 bp in length
      * 6613: gap of unknown length
      * 6713: gap of unknown length
      * 8315: contig of 1602 bp in length
      * 8415: gap of unknown length
      * 9446: contig of 1031 bp in length
      * 9447: gap of unknown length
      * 9547: gap of unknown length
      * 10746: contig of 1200 bp in length
      * 10846: gap of unknown length
      * 12550: contig of 1704 bp in length
      * 12551: gap of unknown length
      * 14042: contig of 1392 bp in length
      * 14043: gap of unknown length
      * 14142: gap of unknown length
      * 15833: contig of 1691 bp in length
      * 15933: gap of unknown length
      * 17376: contig of 1443 bp in length
      * 17377: gap of unknown length
      * 17477: contig of 1191 bp in length
      * 18667: gap of unknown length
      * 18668: contig of 1277 bp in length
      * 20045: gap of unknown length
      * 20144: contig of 1224 bp in length
      * 21368: gap of unknown length
      * 21469: contig of 1314 bp in length
      * 22782: gap of unknown length
      * 22882: contig of 1929 bp in length
      * 24811: gap of unknown length
      * 24812: contig of 1605 bp in length
      * 24912: gap of unknown length
      * 26517: gap of unknown length
      * 26518: contig of 1079 bp in length
      * 26617: gap of unknown length
      * 27696: contig of 2432 bp in length
      * 27796: gap of unknown length
      * 30228: contig of 1719 bp in length
      * 30328: gap of unknown length
      * 32046: contig of 1719 bp in length
      * 32147: gap of unknown length
      * 33361: contig of 1215 bp in length
      * 33461: gap of unknown length
      * 33622: contig of 1224 bp in length
      * 34683: gap of unknown length
      * 34785: contig of 1747 bp in length
      * 34886: gap of unknown length
      * 35332: contig of 1289 bp in length
      * 36633: gap of unknown length
      * 37921: contig of 1289 bp in length
      * 37922: gap of unknown length
      * 38021: contig of 2038 bp in length
      * 40059: gap of unknown length
      * 40159: contig of 1193 bp in length
      * 41352: gap of unknown length
      * 41452: contig of 1323 bp in length
      * 42775: gap of unknown length
      * 42876: contig of 1818 bp in length
      * 44693: gap of unknown length
      * 44794: contig of 2376 bp in length
      * 47169: gap of unknown length
      * 47269: gap of unknown length
      * 47170

```



```

* 47270 48305: contig of 1036 bp in length
* 48306 48405: gap of unknown length
* 48406 50809: contig of 2404 bp in length
* 50810 50909: gap of unknown length
* 50910 52196: contig of 1287 bp in length
* 52197 52296: gap of unknown length
* 52297 54124: contig of 1828 bp in length
* 54125 54224: gap of unknown length
* 54225 57287: contig of 3063 bp in length
* 57288 57387: gap of unknown length
* 57388 59339: contig of 1952 bp in length
* 59340 59439: gap of unknown length
* 59440 62167: contig of 2728 bp in length
* 62168 62267: gap of unknown length
* 62268 65332: contig of 3265 bp in length
* 65333 65632: gap of unknown length
* 65633 68832: contig of 3200 bp in length
* 68833 68932: gap of unknown length
* 68933 73578: contig of 4646 bp in length
* 73579 73678: gap of unknown length
* 73679 79007: contig of 5329 bp in length
* 79008 84346: contig of 5239 bp in length
* 84347 84446: gap of unknown length
* 84447 89756: contig of 5310 bp in length
* 89757 93568: gap of unknown length
* 93569 93668: contig of 3712 bp in length
* 93669 97591: gap of unknown length
* 97592 97691: gap of unknown length
* 97692 102109: contig of 4418 bp in length
* 102110 102209: gap of unknown length
* 102210 115186: contig of 12977 bp in length
* 115187 115286: gap of unknown length
* 115287 126142: contig of 10856 bp in length
* 126143 126242: gap of unknown length
* 126243 140107: contig of 13865 bp in length
* 140108 140207: gap of unknown length
* 140208 150877: contig of 10670 bp in length
* 150878 150977: gap of unknown length
* 150978 200603: contig of 49626 bp in length.

FEATURES             Location/Qualifiers
     source            1..200603
     /organism="Homo sapiens"
     /db_xref="taxon:9606"
     /chromosome="19"
     /clone_lib="Caltech human BAC library D"
     /clone_lib="50919 c 51731 g 46633 t 5014 others"

BASE COUNT  46306 a 50919 c 51731 g 46633 t 5014 others
ORIGIN

alignment_scores:
    Quality: 148.00      Length: 28
    Ratio: 5.286         Gaps: 0
    Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-689-911-2 x AC024580/rev ..
Align seg 1/1 to reverse of: AC024580 from: 1 to: 200603

45 ProValLeuHisLeuProGlnMetGlyAspGlnAspGlyLysArgGluTh 61
127039 CCAGTCTCCACCTCCCAATGGGTGACCAAGACGGAAGAGGGAGAC 126990
6 rLaLeuGluLeuLeuAspLeuTrpLysAlaLeu 72
126984 AGCCCTTGAGATCTAGACCTGTGGAAGGCATC 126956

seq_name: gb_ro:RATGALA
seq_documentation_block:
LOCUS               46306 bp      mRNA      ROD
DEFINITION          Rat galanin mRNA, complete cds.
ACCESSION            M18102
VERSION              M18102.1
KEYWORDS             Galanin.
SOURCE              Rat (strain Fisher 344) pituitary cells, cDNA to mRNA, clone pE1C.
ORGANISM             Rattus norvegicus
                     Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                     Rattus.
REFERENCE            1 (bases 1 to 680)
AUTHORS              Vrontakis, M.E., Peden, L.M., Duckworth, M.L. and Friesen, H.G.
TITLE                Isolation and characterization of a complementary DNA (galanin)
                     clone from estrogen-induced pituitary tumor messenger RNA
JOURNAL              J. Biol. Chem. 262, 16755-16758 (1987)
MEDLINE              88059066
FEATURES             Location/Qualifiers
     source            1..680
     /organism="Rattus norvegicus"
     /db_xref="taxon:10116"
     /note="galanin"
     /protein_id="AAA41187.1"
     /db_xref="GI:204239"
     /translation="MARGSVILLAMLLVATLSATLGLCMPTKEKRGWTLNSAGYLLG
                     PHAIDNHRFSFDKGLTKRELPLEVEGRIGLSVAVLPESNIVRTIMEFLSLHLKE
                     AGALDLPGLPLATSSDLEQS"
BASE COUNT  164 a 199 c 164 g 153 t
ORIGIN

alignment_scores:
    Quality: 104.50      Length: 70
    Ratio: 2.322         Gaps: 2
    Percent Similarity: 64.286      Percent Identity: 41.429

alignment_block:
US-09-689-911-2 x RATGALA ..
Align seg 1/1 to: RATGALA from: 1 to: 680

1 MetAlaProSerValProLeuValLeuValLeuValLeuValLeuSe 17
125 ATGGCCAGGGCGAGCGTTATCTGCTAGCTGCTGCTCTGTTGCAAC 174
17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyL 34
175 CCTGTGAGCCACTCTGGGGCTGGGATGCCAACAAAGAGAGAGAGCT 224
34 rPThrLeuAsnSerAlaGlyTyrLeuLeuGlyPro.....ValLeuHis 48
225 GGACCCCTGAACAGCGCTGCTACCTTCTGGGGCCCATGCCATTGACA 274
49 LeuProGlnMetGlyAspGln.....AspGlyLysArgGluThral 62
275 CACAGATCATTTAGCGACAAGCATGGCTGCACAGCAAGAGAGGAGTACC 324
62 aLeuGluLeu 65
325 ACTGGAAGTG 334

seq_name: gb_ro:RATGALA
seq_documentation_block:
LOCUS               699 bp      mRNA      ROD
DEFINITION          Rat galanin (a neuropeptide) mRNA, complete cds.
ACCESSION            J03624
VERSION              J03624.1
KEYWORDS             galanin; neuropeptide Y.
SOURCE              Rat (Sprague-Dawley) hypothalamus, cDNA to mRNA, (library of
                     R.Goodman), clones rg-[2,5].
ORGANISM             Rattus norvegicus

```



```

*      38565 39303: contig of 739 bp in length
*      39304 39403: gap of 100 bp
*      39404 40155: contig of 752 bp in length
*      40156 40255: gap of 100 bp
*      40256 41019: contig of 764 bp in length
*      41020 41119: gap of 100 bp
*      41120 41861: contig of 742 bp in length
*      41862 41961: gap of 100 bp
*      41962 42727: contig of 766 bp in length
*      42728 42827: gap of 100 bp
*      42828 43564: contig of 737 bp in length
*      43565 43664: gap of 100 bp
*      43665 44421: contig of 757 bp in length
*      44422 44521: gap of 100 bp
*      44522 45258: contig of 737 bp in length
*      45259 45358: gap of 100 bp
*      45359 46103: contig of 745 bp in length
*      46104 46203: gap of 100 bp
*      46204 46943: contig of 740 bp in length
*      46944 47043: gap of 100 bp
*      47044 47742: contig of 699 bp in length
*      47743 47842: gap of 100 bp
*      47843 48584: contig of 742 bp in length
*      48585 48684: gap of 100 bp
*      48685 49430: contig of 746 bp in length
*      49431 49530: gap of 100 bp
*      49531 50287: contig of 757 bp in length
*      50288 50387: gap of 100 bp
*      50388 51143: contig of 756 bp in length
*      51144 51243: gap of 100 bp
*      51244 52004: contig of 761 bp in length
*      52005 52104: gap of 100 bp
*      52105 52857: contig of 753 bp in length
*      52858 52957: gap of 100 bp
*      52958 53690: contig of 733 bp in length
*      53691 53790: gap of 100 bp
*      53791 54504: contig of 714 bp in length
*      54505 54604: gap of 100 bp
*      54605 55309: contig of 705 bp in length
*      55310 55409: gap of 100 bp
*      55410 56154: contig of 745 bp in length
*      56155 56254: gap of 100 bp
*      56255 56976: contig of 722 bp in length
*      56977 57076: gap of 100 bp
*      57077 57817: contig of 741 bp in length
*      57818 57917: gap of 100 bp

alignment_scores:
Quality: 101.50      Length: 111
Ratio: 1.637        Gaps: 4
Percent Similarity: 55.856      Percent Identity: 32.432

alignment_block:
US-09-689-911-2 x AC087454 ..

Align seg 1/1 to: AC087454 from: 1 to: 66256

14 LeuLeuSerLeuAlaGluThrProAlaSerAlaProAlaHisArgG1 30
||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
42214 CTCTGGGAGCAGCCAGCCAGGAGCCAGCTCGGTCGCCAGCAGAGTG 42263

30 YArgGlyGlyTrpThrLeuAsnSerAlaGlyTyrLeuLeuGlyProValL 47
||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
42264 AAGCAGAGAGTGGGGCTCAGGGCTCGAGGC.....CTTGCGGTGCC 42307

47 euHisLeuProGlnMetGly.....AspGlnAspGlyLys 58
||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
42308 TTGAGAGCCCTTGGATGGGCACTCAGGCCCCCATGTCCAGCAGGGCCCT 42357

59 ArgGluThrAlaLeuGluLeuLeuAspLeuTrpLysAlaLeuAspGlyLe 75
||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
42358 AGGGAGGTAGGCATTGAGCAGAGGGGCCCTTTGGAGG.....TGGGG 42398

```

```

*      8244 8343: gap of 100 bp
*      8344 9091: contig of 748 bp in length
*      9092 9191: gap of 100 bp
*      9192 9934: contig of 743 bp in length
*      9935 10034: gap of 100 bp
*      10035 10794: contig of 760 bp in length
*      10795 10894: gap of 100 bp
*      10895 11601: contig of 707 bp in length
*      11602 11701: gap of 100 bp
*      11702 12439: contig of 738 bp in length
*      12440 12539: gap of 100 bp
*      12540 13299: contig of 760 bp in length
*      13300 13399: gap of 100 bp
*      13400 14155: contig of 756 bp in length
*      14156 14255: gap of 100 bp
*      14256 14985: contig of 730 bp in length
*      14986 15085: gap of 100 bp
*      15086 15830: contig of 745 bp in length
*      15831 15930: gap of 100 bp
*      15931 16661: contig of 731 bp in length
*      16662 16761: gap of 100 bp
*      16762 17487: contig of 726 bp in length
*      17488 17587: gap of 100 bp
*      17588 18350: contig of 763 bp in length
*      18351 18450: gap of 100 bp
*      18451 19171: contig of 721 bp in length
*      19172 19271: gap of 100 bp
*      19272 20016: contig of 745 bp in length
*      20017 20116: gap of 100 bp
*      20117 20860: contig of 744 bp in length
*      20861 20960: gap of 100 bp
*      20961 21686: contig of 726 bp in length
*      21687 21786: gap of 100 bp
*      21787 22540: contig of 754 bp in length
*      22541 22640: gap of 100 bp
*      22641 23382: contig of 742 bp in length
*      23383 23482: gap of 100 bp
*      23483 24239: contig of 757 bp in length
*      24240 24339: gap of 100 bp
*      24340 25073: contig of 734 bp in length
*      25074 25173: gap of 100 bp
*      25174 25901: contig of 728 bp in length
*      25902 26001: gap of 100 bp
*      26002 26743: contig of 742 bp in length
*      26744 26843: gap of 100 bp
*      26844 27559: contig of 716 bp in length
*      27560 27659: gap of 100 bp
*      27660 28403: contig of 744 bp in length
*      28404 28503: gap of 100 bp
*      28504 29220: contig of 717 bp in length
*      29221 29320: gap of 100 bp
*      29321 30041: contig of 721 bp in length
*      30042 30141: gap of 100 bp
*      30142 30896: contig of 755 bp in length
*      30897 30996: gap of 100 bp
*      30997 31764: contig of 768 bp in length
*      31765 31864: gap of 100 bp
*      31865 32579: contig of 715 bp in length
*      32580 32679: gap of 100 bp
*      32680 33414: contig of 735 bp in length
*      33415 33514: gap of 100 bp
*      33515 34278: contig of 764 bp in length
*      34279 34378: gap of 100 bp
*      34379 35119: contig of 741 bp in length
*      35120 35219: gap of 100 bp
*      35220 35965: contig of 746 bp in length
*      35966 36065: gap of 100 bp
*      36066 36785: contig of 720 bp in length
*      36786 36885: gap of 100 bp
*      36886 37636: contig of 751 bp in length
*      37637 37736: gap of 100 bp
*      37737 38464: contig of 728 bp in length
*      38465 38564: gap of 100 bp

```

```
75 uProTy-SerHisProGlnProSerLysArgAsnValMetGluThrp 92
|||||
42399 TCCTGAAGCTGGAGGACCGGGACCAAGCAGGAGCGGTGTGAGCGTGGG 42448
92 heAlaLysProGluIleGlyLysAlaArgLysHisArgGluThr 108
|||||
42449 GGTACAGCCGAGGCGTGTGTGGAGAGG..... 42480
109 ProThrGlyGluGlyGluGlnGlySerGlyArg 119
|||||
42481 ...GGAGGAGAGGCCAAGTCAGAGCGGCGCAGG 42510
seq_name: gb_htg:AC073548
seq_documentation_block:
LOCUS AC073548 170537 bp DNA HTG 26-JUL-2001
DEFINITION Homo sapiens chromosome 19 clone RP11-43N16, *** SEQUENCING IN
PROGRESS ***, 3 ordered pieces.
ACCESSION AC073548
VERSION AC073548.4 GI:15022024
KEYWORDS HTG: HTGS_PHASE2; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Unpublished
2 (bases 1 to 170537)
DOE Joint Genome Institute.
Direct Submission
Submitted (22-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 26, 2001 this sequence version replaced gi:13699754.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as runs of N. However the sizes
* of the gaps between them are given, however the sizes
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 66051: contig of 66051 bp in length
* 56052 66151: gap of unknown length
* 66152 67688: contig of 1537 bp in length
* 67689 67789: gap of unknown length
* 67789 170537: contig of 102749 bp in length.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 423205
Center clone name: RP11-43N16
-----
Summary Statistics
Consensus quality: 167142 bases at least Q40
Consensus quality: 168091 bases at least Q30
Consensus quality: 168171 bases at least Q20
Estimated insert size: 168000; agarose-fp estimation
Estimated insert size: 168346; sum-of-contigs
estimation
Quality coverage: 9.86 in Q20 bases; agarose-fp
estimation
Quality coverage: 9.83 in Q20 bases; sum-of-contigs
estimation.
Location/Qualifiers
1..170537
/organism="Homo sapiens"
/db_xref="taxon:9606"
FEATURES
source
```

```
/chromosome="19"
/clone="RP11-43N16"
BASE COUNT 39169 a 47124 c 44400 g 39641 t 203 others
ORIGIN
alignment_scores:
Quality: 101.50 Length: 111
Ratio: 1.637 Gaps: 4
Percent Similarity: 55.856 Percent Identity: 32.432
alignment_block:
US-09-689-911-2 x AC073548 ..
Align seg 1/1 to: AC073548 from: 1 to: 170537
14 LeuLeuSerLeuAlaGluThrProAlaSerAlaProAlaHisArgG1 30
|||||
48767 CTTCTGGGACCAAGGCCAGGAGCCAGCTCGGTCGCCAGGCGAGGTG 48816
30 yArgGlyGlyThrLeuAsnSerAlaGlyThrLeuLeuGlyProValL 47
|||||
48817 AAGCGAAGTGGGCTCAGGCGCTGGAGGC.....CTGCCGCTGCC 48860
47 euHisLeuProGlnMetGly.....AspGlnAspGlyLys 58
|||||
48861 TTGAGAGCCCTTGGATGGGCATCAGGCCCATGTCCAGCAGGCGCCT 48910
59 ArgGluThrAlaLeuGluIleLeuAspLeuTrpLysAlaIleAspGly 75
|||||
48911 AGGAGGTGAGCATGTGACGAGGCGCTTTGGAGG.....TGGGG 48951
75 uProTy-SerHisProGlnProSerLysArgAsnValMetGluThrp 92
|||||
48952 TCCTGAAGCTGGAGGACCGGGACCAAGCAGGAGCGGTGTGAGCGTGGG 49001
92 heAlaLysProGluIleGlyLysAlaArgLysHisArgGluThr 108
|||||
49002 GGTACAGCCGAGGCGTGTGTGGAGAGG..... 49033
109 ProThrGlyGluGlyGluGlnGlySerGlyArg 119
|||||
49034 ...GGAGGAGAGGCCAAGTCAGGAGCGGCGCAGG 49063
seq_name: gb_pat:A28025
seq_documentation_block:
LOCUS A28025 575 bp DNA PAT 25-SEP-1995
DEFINITION Human preprogalanin cDNA sequence.
ACCESSION A28025
VERSION A28025.1 GI:1247489
KEYWORDS human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 575)
HUMAN GALANIN, cDNA CLONES ENCODING HUMAN GALANIN AND A METHOD OF
PRODUCING HUMAN GALANIN
Patent: WO 9215681-A 5 17-SEP-1992;
Location/Qualifiers
1..575
/organism="Homo sapiens"
/db_xref="taxon:9606"
14..385
/codon_start=1
/product="galanin"
/protein_id="CAA01907.1"
/db_xref="GI:1247490"
/translation="MARGSALLASLLAAALASAGLSAPAKRGWTLNSAGYLLG
PHAVGNHRSFSDKNGLTSKRELPRDDMKPGSFDRIIPENNIMRTIIEFLSFHLKEA
GALDRLDLLPAAASSEDIDERS"
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
```

```

32 CTCCTGCTCGCTCCCTCTCTCTCGCGCGGCCCTTTTCGCTCTGCGGG 81
26 .....ProAlaHisArgGlyArgGlyGlyTyrThrLeuAsnSerA 39
      ||||| : : : |||||
82 GCTCTGTCGCCGGCCAGGAAAACGA...GGCTGGACCCCTGAACACGC 128
39 lagTyrLeuLeuGlyPro.....ValLeuHisLeuProGlnMetGly 53
      ||||| ||||| ||||| : : : : : : : : :
29 CGGCTTACCTGCTGGGCCACATGCGTTGGCAACACACAGGTCATTTCAGC 178
54 AspGlnAspGly.....LysArgGluThrAlaLeuGluIleLeuAs 67
      ||||| : : : ||||| |||||
179 GACAGNATGGCCTACCAGCAAGCGGGAGCTCGCGCCCGAA..... 220
67 pLeuTrpLysAlaIleAspGlyLeuProTyrSerHisProProGlnProS 84
      ||||| ||||| ||||| : : :
221 .....GATGACATGATGAACACGAGGAGCTTTGACAGGTCCATAC 257
84 erLysArgAsnValMetGluThr 91
      : : : : : : : : : : : : : : :
258 CTGAAACAATATCATCGGCACA 280

```

BASE COUNT	128 a	162 c	140 g	145 t
ORIGIN				

alignment_scores:		
Quality:	99.50	91
Ratio:	1.951	5
Percent Identity:	56.044	
		Percent Identity: 41.758

```
alignment_block:
  MS-09-689-911-2 x A28025  ..
```

align seq 1/1 to: A28025 from: 1 to: 575

```

10 LeuLeuValLeuLeuSerLeuAlaGluThrProAlaSerAla.. 25
   |||||:::|||||:::|||||
33 CTCTGTGGCCCTCCTCTCTCGCGGGCCCTTTCCTGCGGG 81
   |||||:::|||||:::|||||
26 .....ProAlaHisArgYarGlyGlyTrpThrLeuAsnSerA 39
   |||||:::|||||:::|||||
82 GCTCTGTGTGCGCGCAAGAAAAACA...GGCTGGACCTTGAAACGC 128
   |||||:::|||||:::|||||
39 laGlyTyrLeuLeuGlyPro.....ValLeuHisLeuProGlnMetGly 53
   |||||:::|||||:::|||||
129 CGGCTACCTGCTGGGCCCATCGCTTGGCAACCAGGTTCATTCAGC 178
   |||||:::|||||:::|||||
54 AspGlnAspGly.....LysArgGluThrAlaLeuGluIleLeuAs 67
   |||||:::|||||:::|||||
179 CACAAGAATGGCCTCACACAGCAGCGGAGCTCGCGCCCGAA... 220
   |||||:::|||||:::|||||
67 pleuTrpLysAlaIleAspGlyLeuProTyrSerHisProGlnProS 84
   |||||:::|||||:::|||||

```

84 erLysArgAsnValMetGluThr 91  
:::|||||:::|||||  
258 CTGAAACAAATATCATGCGCACA 280

seq\_name: qb\_pat:AR009787

seq_documentation_block:		DNA	PAT
LOCUS	AR009787	575 bp	
DEFINITION	Sequence 8 from patent	US 5756460.	
ACCESSION	AR009787		
VERSION	AR009787.1	GI:3968592	
KEYWORDS	.		
SOURCE	Unknown.		

UNCLASSIFIED  
 (Dates 1 to 575)  
 Evans, H. Frances and Shine, J.  
 Human galanin, cDNA clones encoding human galanin and a method of  
 producing human galanin  
 Patent: US 5756460-A 8 26-MAY-1998;  
 Location/Qualifiers  
 1. 575

	128 a	162 c	140 g	145 t
BASE COUNT				
ORIGIN				

alignment_scores:		
Quality:	99.50	Length: 91
Ratio:	1.951	Gaps: 5
Percent Similarity:	56.044	Percent Identity: 41.758

```
alignment_block: 0000789
```

11-2000 1/1 to: AR009787 from: 1 to: 575

10 LeuLeuLeuValLeuLeuLeuSerLeuAlaGluThrProAlaSerAla.. 25  
|||||||... |||||

Mon Mar 4 11:27:01 2002

us-09-689-911-2.rge

Page 12



```
32 CTCCTGCTGCTGCCCTCCCTCCTCGCCGCGCCCTTCTGCTGCTGCGGG 81
26 .....ProAlaHisArgGlyArgGlyGlyThrLeuAsnSerA 39
82 GCTCTGCTGCGCCGCGCAAGGAACGA...GGCTGGACCTGACACGG 128
39 laGlyTyrLeuLeuGlyPro.....ValLeuHisLeuProGlnMetGly 53
129 CGGCTACCTGCTGCGCCCATCGCTTGGCAACCAACAGGTCAATCAGC 178
54 AspGlnAspGly.....LysArgGluThrAlaLeuGluLeuLeuAs 67
179 GACAAGATGGCTCACCACGACGCGGAGCTGCGGCCGAA..... 220
67 pLeuTyrLysAlaLeuAspGlyLeuProTyrSerHisProGlnProS 84
221 .....GATGACATGAACACGGAAGCTTTCACAGGTCCATAC 257
84 erLysArgAsnValMetGluThr 91
258 CTGAACAACAATATCATGCGCA 280

seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-916-917-1

seq_documentation_block:
; Sequence 1, Application US/08916917
; Patent No. 5856132
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip Thomas
; APPLICANT: Braselmann, Sylvia
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3, KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,917
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 8549-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-916-917-1
```

```
alignment_scores:
Quality: 85.50
Ratio: 1.474
Length: 109
Gaps: 6
```

```
Percent Similarity: 53.211 Percent Identity: 32.110
alignment_block:
US-09-689-911-2 x US-08-916-917-1 ..
Align seg 1/1 to: US-08-916-917-1 from: 1 to: 4692
21 ThrProAlaSerAlaProAla.HisArgGlyArgGly.....GlyTrpT 35
1879 ACAGCGCCGCCGCCCTTCTCTGAGCGGGACGAGGACCCCAAGGCTTCC 1928
35 hrLeuAsnSerAlaGlyTyrLeuLeu.....Gly 44
1929 ACCTGCGTGTCTGCTGCTTCGCTCGGATCGGGGAAGGTGGT 1978
45 ProValLeuHisLeuPro...GlnMetGlyAspGlnAspGlyLysArgGl 60
1979 CCGGGCTTACAGCAACCTCGCGCGGCTGGAGAACACACCGTCTCTCCTCA 2028
60 uThrAlaLeuGluLeuAspLeuTyrLysAlaLeuAspGlyLeuProT 77
2029 CACGGTCTCTAAGTACAGTCTTCTACGTGCTGTCAAGCGGAGCGGT 2078
77 yrSer.....HisProGlnProSerLysArgAsnValMetGlu 90
2079 GGGACAGGCAACCCCAACAGCCAGCCCTCGGAGCCAGACGCCGCCCT 2128
91 ThrPheAlaLysProGluLeuGlyLysAlaArgLysHisArgGl 107
2129 CCCCACAGACGCCCGGACCCCGGCGCTGCAGAGCTGGGCGCGCGC.. 2176
107 uThrProThrGlyGluGluGln 115
2177 ....CCCTGGGAGGAGAGACCAA 2197

seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-972-631-1

seq_documentation_block:
; Sequence 1, Application US/08972631
; Patent No. 5856133
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3, KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,631
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 8549-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-3660
; TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 1:
```



us-09-689-911-2.rni

Mon Mar 4 11:27:02 2002

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-972-631-1

alignment_scores:
  Quality: 85.50      Length: 109
  Ratio: 1.474      Gaps: 6
  Percent Similarity: 53.211      Percent Identity: 32.110

alignment_block:
  US-09-689-911-2 x US-08-972-631-1 ..
  Align seg 1/1 to: US-08-972-631-1 from: 1 to: 4692

21 ThrProAlaSerAlaProAla.HisArgGlyArgGly.....GlyTrpT 35
1879 ACCAGCGCGCGCCCTTCTGTAGCGGGGACGAGACCCCAAGGCTTCC 1928
35 hrLeuAsnSerAlaGlyTyrLeuLeu.....Gly 44
1929 ACGTGTCTGTCTGTCTTCTCGGCTCGGATCTCGGGGAAGTGGT 1978
45 ProValLeuHisLeuPro...GlnMetGlyAspGlnAspGlyLysArgG1 60
1979 CCGGGCTTACAGCAACCTCGCGCGGTGGAGAACACCGCTCTCTCTCA 2028
60 uThrAlaLeuGluLeuAspLeuTyrLysAlaLeuAspGlyLeuProT 77
2029 CACGGTCTTCAAGTACAGTCTTCTACGTGCTGTCAAGCGGAGCGGT 2078
77 yrSer.....HisProGlnProSerLysArgAsnValMetGlu 90
2079 GGGACAGGCACCCACAGCCCGCTCGGAGCCACGACGCCCCCCT 2128
90 ThrPheAlaLysProGluLeuGlyLysAlaArgLysHisArgG1 107
2129 CCCACAGACGCGCCGAGGACCCCGGCGCTCGAGAGTGGGCGCGC... 2176
107 uThrProThrGlyGluGlyGluGln 115
2177 ....CCCTGGGAGGAGACCAAA 2197

seq_name: /cgn2_5/ptodata/1/ina/5B_COMB.seq:US-08-972-629-1

seq_documentation_block:
; Sequence 1, Application US/08972630
; Patent No. 5859201
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Stephens, Len
; APPLICANT: Stephens, Len
; TITLE OF INVENTION: G-BETA-CAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,629
; FILING DATE:

```

```

; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,630
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 8549-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-3660
; TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-972-630-1

```

```

alignment_scores:
  Quality: 85.50      Length: 109
  Ratio: 1.474       Gaps: 6
  Percent Similarity: 53.211  Percent Identity: 32.110

```

```
alignment_block:
US-09-689-911-2 x US-08-972-630-1 ..

```

```
Align seg 1/1 to: US-08-972-630-1 from: 1 to: 4692

```

```

21 ThrProAlaSerAlaProAla.HisArgGlyArgGly.....GlyTrpT 35
||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1879 ACCAGCGCGCGCGCGCGCTTCTGAGCGGGGACGAGGACCCCAAGGCTTC 1928
35 hrLeuAsnSerAlaGlyTyrLeuLeu.....Gly 44
||| |||
1929 ACGTCGCGTGTCTGCTTCTCGGCTCGGATCTCGGGGAAGGTGGT 1978
45 ProValLeuHisLeuPro...GlnMetGlyAspGlnAspGlyLysArgG1 60
||| |||:|||||:|||||:|||||:|||||:|||||:|||||:
1979 CCGGGCTTACAGCAACCTCGCGCGGCTGGAGAACACACCTCTCTCTCA 2028
60 uThrAlaLeuGluLeuLeuAspLeuTrpLysAlaLeuAspGlyLeuProT 77
|||:|||||:|||||:|||||:|||||:|||||:|||||:
2029 CACGGTTCTTCAAGCTACAGTTCTTCTAGTCGCTGTCAAGCGGAGCCGT 2078
77 yrSer.....HisProGlnProSerLysArgAsnValMetGlu 90
|||:|||||:|||||:|||||:|||||:|||||:|||||:
2079 GGGACAGGACCCCGGAGCGCGCTCGGAGCAACGCGCCCGCT 2128
91 ThrPheAlaLysProGluLeuGlyLysAlaArgLysHisArgArgG1 107
|||:|||||:|||||:|||||:|||||:|||||:|||||:
2129 CCCCACAGACGCGCGGAGGACCCCGGCGCTCGACAGCTGGCGCGCG... 2176
107 uThrProThrGlyGluGlyGluGln 115
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
217 .....CCCTGGGAGGAGACCA 2197

```

```
seq_name: /cgn2_6/ptodata/1/ina/5B_comb.seq:US-08-672-211-1

```

```

seq_documentation_block:
; Sequence 1, Application US/08672211
; Patent No. 5874273
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-CAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,211
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 8549-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-3660
; TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-672-211-1

```

```

alignment_scores:
  Quality: 85.50      Length: 109
  Ratio: 1.474       Gaps: 6
  Percent Similarity: 53.211  Percent Identity: 32.110

```

```
alignment_block:
US-09-689-911-2 x US-08-672-211-1 ..

```

```

Align seg 1/1 to: US-08-672-211-1 from: 1 to: 4692
21 ThrProAlaSerAlaProAla.HisArgGlyArgGly.....GlyTrpT 35
||| |||:|||||:|||||:|||||:|||||:|||||:|||||:
1879 ACCAGCGCGCGCGCGCTTCTGAGCGGGGACGAGGACCCCAAGGCTTC 1928
35 hrLeuAsnSerAlaGlyTyrLeuLeu.....Gly 44
||| |||
1929 ACGTCGCGTGTCTGCTTCTCGGCTCGGATCTCGGGGAAGGTGGT 1978
45 ProValLeuHisLeuPro...GlnMetGlyAspGlnAspGlyLysArgG1 60
||| |||:|||||:|||||:|||||:|||||:|||||:
1979 CCGGGCTTACAGCAACCTCGCGCGGCTGGAGAACACACCTCTCTCTCA 2028
60 uThrAlaLeuGluLeuLeuAspLeuTrpLysAlaLeuAspGlyLeuProT 77
|||:|||||:|||||:|||||:|||||:|||||:|||||:
2029 CACGGTTCTTCAAGCTACAGTTCTTCTAGTCGCTGTCAAGCGGAGCCGT 2078
77 yrSer.....HisProGlnProSerLysArgAsnValMetGlu 90
|||:|||||:|||||:|||||:|||||:|||||:|||||:
2079 GGGACAGGACCCCGGAGCGCGCTCGGAGCAACGCGCCCGCT 2128
91 ThrPheAlaLysProGluLeuGlyLysAlaArgLysHisArgArgG1 107

```

```

2129 CCCACAGACCCCGAGGACACCGGGCCCTGCAGAGCTGGGCGCCGC.. 2176
      ::::|||||      |||      ::::|||||      |||||||
107 uThrProThrGlyGluGlyGln 115
      |||      |||      ::::|||||
2177 ....CCCTGGGAGGAGGACACCAA 2197
      ::::|||||      |||      ::::|||||

seq_name: /cgn2.6/ptodata/1/ina/6A_COMB.seq:US-09-225-170-1
seq_documentation_block:
Sequence 1, Application US/09225170
Patent No. 6017763
GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip Thomas
APPLICANT: Braselmann, Sylvia
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3, KINASE

```

```

1 NUMBER OF SEQUENCES: 14
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: Pennie & Edmonds, LLP
4 STREET: 1155 Avenue of the Americas
5 CITY: New York
6 STATE: NY
7 COUNTRY: USA
8 ZIP: 10036-2811
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: Diskette
11 COMPUTER: IBM Compatible
12 OPERATING SYSTEM: Windows
13 SOFTWARE: FastSeq for Windows Version 2.0b
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/09/225,170
16 FILING DATE:
17 CLASSIFICATION:
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: 08/916,917
20 FILING DATE: 15-AUG-1997
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Abrams, Samuel B
23 REGISTRATION NUMBER: 30,605
24 REFERENCE/DOCKET NUMBER: 8549-0006-999
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: 650-493-4935
27 TELEFAX: 650-493-5556
28 TELEX: 66141 PENNIE
29 INFORMATION FOR SEQ ID NO: 1:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 4692 base pairs
32 TYPE: nucleic acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35 US-09-225-170-1
36
37 alignment_scores:
38     Quality: 85.50
39     Ratio: 1.474
40     Percent Similarity: 53.211
41
42 alignment_block:
43     Length: 109
44     Gaps: 6
45     Percent Identity: 32.110

```

Align seg 1/1 to: US-09-225-170-1 from: 1 to: 4692

21 ThrProAlaSerAlaProAla.HisArgGlyArgGly.....GlyTrpT 35  
||| |||||:|||||:|||||:|||||:  
1879 ACAGCGGCCGCCCCCTTCCTGAGCGGGCAGGAGCCCCAAGSGTTCC 191  
  
35 hrLeuAsnSerAlaGlyTyrLeuLeu.....Gly 44  
||| |||||  
1929 ACGTGACGTGTCGTGGTCTTCGGCTCGGATCTCGGGAGGTGET 191



us-09-689-911-2.rni

Mon Mar 4 11:27:02 2002

```

alignment_scores:
  Quality: 78.00      Length: 134
  Ratio: 1.393      Gaps: 6
  Percent Similarity: 41.791      Percent Identity: 26.119

alignment_block:
  US-09-689-911-2 x US-08-556-419-13/rev ..

Align seg 1/1 to reverse of: US-08-556-419-13 from: 1 to: 10348

16 LeuSerLeuAlaGluThrProAlaSerAla.....ProAlaHi 28
   ||| :|||:|||||:|||||
9804 CTTCAAAGGCTCCGGCCCGCAGCTCCGCTCAGAGTCTCTCCACCACATG 9755
   |||:|:|||||
28 sArgGlyArgGlyGly..... 33
   |||:|:|||||
9754 GCGCTCAGCAGGTGGTGACATTTGTTGACATTTGTTAAACAAGTCAGCAGC 9705
   |||:|:|||||
34 .....TrpThrLeuAsnSerAlaGlyTyrLeuLeu... 43
   |||:|:|||||
9704 CGGTGATATGGGCTTCCTGGGGCTGCACACCTCAAGCACAGACTGGAA 9655
   |||:|:|||||
44 GlyProValLeuHisLeu.....ProGlnMetG1 53
   |||:|:|||||
9654 GGCCTTCGGCTCGAGCTCCCTCTATCTGTGTCTGTAGAGTCTGTGG 9605
   |||:|:|||||
53 yAspGlnAspGlyLysArgGluThrAlaLeuGluLeuLeuAspLeuTrpL 70
   |||:|:|||||
9604 CGACACAGGAGAAAGGTTCCAGTCCACCTG..... 9574
   |||:|:|||||
70 ySalalLeuAspGlyLeuProTyrSerHisProGlnProSerLysArg 86
   |||:|:|||||
9573 .....CTCCAGCTTGCCTATCTCTGTAT..... 9550
   |||:|:|||||
87 AsnValMetGluThrPheAlaLysProGluLeuGlyGlyLysAlaArgLy 103
   |||:|:|||||
9549 GACATGTGGGAGGATCGCCGACCCAGCGGCTGTGTGACCGCTGACAA 9500
   |||:|:|||||
103 sHisArgArgGluThrProThrGlyGluGluGlnGlySerGlyArgG 120
   |||:|:|||||
9499 AGAAGCAGGAGAGGCTCCAGCTGGCCATGGCGACCGGGGCCCTCTGCGTG 9450
   |||:|:|||||
120 ln 120
   ::
9449 AA 9448

seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-556-419-13

seq_documentation_block:
; Sequence 13, Application US/08556419C
; Patent No. 6093549
; GENERAL INFORMATION:
; APPLICANT: Ross, Christopher
; APPLICANT: Li, Xiao-Jiang
; APPLICANT: Li, Shi-Hua
; APPLICANT: Sharp, Alan
; APPLICANT: Lanahan, Anthony
; APPLICANT: Worley, Paul
; APPLICANT: Snyder, Solomon
; TITLE OF INVENTION: Huntingtin-associated protein
; FILE REFERENCE: 01107.52271
; CURRENT APPLICATION NUMBER: US/08/556,419C
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 10348
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-08-556-419-13

```

```

; APPLICANT: Ambrose, Christine M.
; APPLICANT: Duyao, Mabel P.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Huntington DNA, Protein And Uses Thereof
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246, 982A
; FILING DATE: May 20, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge, A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0609.3880002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 316..9748
; US-08-246-982A-5

alignment_scores:
      Quality: 78.00      Length: 134
      Ratio: 1.393      Gaps: 6
      Percent Similarity: 41.791      Percent Identity: 26.119

alignment_block:
US-09-689-911-2 x US-08-246-982A-5/rev ..

Align seg 1/1 to reverse of: US-08-246-982A-5 from: 1 to: 10366

16 LeuSerLeuAlaGluThrProAlaSerAla.....ProAlaHi 28
||| ||| ::|||::|||
9804 CTTCCAAGGCTCGGGCCCGCCAGCTGCCGCTCACAGTCTCTCCCAACCATG 9755

28 sArgGlyVarGlyGly..... 33
|||::| |||||

9754 GCGCTACGAGGTGGTGCACCTTGTGGAGATTTCGTAAACAAGTCAGCAGC 9705

34 .....TrpThrLeuAsnSerAlaGlyTyrLeuLeu... 43
||| ||| ::|||

9704 CGGTGATATGGGCTTCCTGGGCTGCAACACCCTCAAGCAGACTGGAA 9655

44 GlyProValLeuHisLeu.....ProGlnMetG1 53
|||::|::|::|::|::|::|

9654 GGCCCTCGGCTCGAGCTCCCTCTACTGTGTGTGTAGAAAGTCTGTGG 9605

53 yAspGlnAspGlyLysArgGluThrAlaLeuGluIleLeuAspLeuTrpL 70
||| ||| ::|||

9604 CGACCAGGCAGAAAAGGTTTCAGCTCCACCTG..... 9574

70 ysaIaIleAspGlyLeuProTyrSerHisProGlnProSerLysArg 86
||| ::|||::|::|::|::|::|

9573 .....CTCCAGTGGCCCATCTGCTGAT..... 9550

```

, c /-t-d-t-n / i-ne /6B COMB seq: IIS-08-905-223-203

```

seq_documentation_block:
; Sequence 203, Application US/08905223
; Patent No. 622029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Dueltel, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 203:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: DOUBLE
; TOPOLOGY: LINEAR
;

```

ZIP: 20005

```

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 51A
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R., 203
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3880003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 316..9748
US-08-453-265-5

alignment_scores:                               Length:   134
Quality:    78.00                                Gaps:      6
Ratio:     1.393                                Percent Identity: 26.119
Percent Similarity: 41.791

alignment_block:
US-09-689-911-2 x US-08-453-265-5/rev ..

Align seg 1/1 to reverse of: US-08-453-265-5 from: 1 to: 10366
16 LeuserLeuAlaGluThrProAlaSerAla.....ProAlaHi 28
||||| :|||:|||||:::|||
||||| :|||:|||||:::|||

```

```

alignment_scores:
  Quality: 77.50      Length: 144
  Ratio: 1.174      Gaps: 8
  Percent Similarity: 45.833      Percent Identity: 31.944

alignment_block:
  US-09-689-911-2 x US-08-905-223-203      ..

  Align seg 1/1 to: US-08-905-223-203 from: 1 to: 491

6 ValProLeuValLeuLeuLeuValLeuLeuLeuSerLeuAlaGluThrPr 22
|||||::: |||||||:::|||||:::
51 GTCCCACTCTCGAGTGTGTGGTGCTCTTACCTT..... 88
22 oAlaSerAlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerA 39
|||||::: |||||||:::|||||:::
89 .....GCCCTGACCTCATGGC.....TCGTG 110
39 laGlyTyrLeuLeuGlyProVal.....LeuHisLeuPro..... 50
|||||::: |||||||:::|||||:::
111 CTGGCTGTCTGGCAGCCCTGTGCAAAAGCTACTTCCCTACCTGATGGC 160
51 .....GlnMetGlyAspGlnAspGlyLysArgGluThr....Al 62
||| |||||||:::|||||:::
161 CGTGCTGACTCCCAAGACACCGCAAGATGGAGAGCAAGAACGGAGC 210
||| |||
62 aLeuGluIleLeuAspLeuTyrLysAlaIleAspGlyLeuProTyrSerH 79
|||
211 TCCT..... 214
79 IsProGlnProSerLysArgAsnValMetGluThrPheAlaLysPro 95
|||||:::|||||:::
215 .....CACCCAGATAAA..... 226
96 GluIleGlyLysAlaArgLysHisArgArgGluThrProThrGlyGl 112
||| |||::: |||::: |||::: |||::: |||::: |||:::
227 .....GGGGTTACAGGAGGCTCCGGGAAGTGGCCCTACTGGAGC 267
112 uGlyGluGlnGlySerGlyArgGlnSerLeuGluAspLeuGlyMetLys 129
||| |||::: |||::: |||::: |||::: |||::: |||:::
268 TGGGCTCGGAACCGGAGCCAACTTTCAGTCTTACCACCGGG...CTGC 314
129 erMetLysIleProLysGluGluAspValLeu 139
:: |||::: |||::: |||::: |||::: |||::: |||:::

```



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2002, 22:17:19 ; Search time 154.9 Seconds  
(without alignments)  
2357.783 Million cell updates/sec

Title: US-09-689-911-1  
Perfect score: 426  
Sequence: 1 atggctctctccctccgtccc.....aagatgctctgaagtcataag 426

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues  
Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_1101.\*  
1: /SIDSI/gcgdata/geneseq/geneseq/NA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseq/NA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq/NA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseq/NA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseq/NA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseq/NA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseq/NA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseq/NA1987.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseq/NA1988.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseq/NA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseq/NA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseq/NA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseq/NA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseq/NA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseq/NA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseq/NA1995.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseq/NA1996.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseq/NA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseq/NA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseq/NA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseq/NA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseq/NA2001.DAT.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	426	100.0	426	22 AAD04547	Galanin family pro
2	296.4	69.6	351	22 AAD04548	Galanin family pro
3	296.4	69.6	473	20 AAZ25536	Receptor binding p
4	184.2	43.2	974	20 AAZ25530	pGR2PL6 cDNA seque
5	183.6	43.1	695	20 AAZ25535	Receptor binding p
6	180	42.3	180	20 AAZ25534	Receptor binding p
7	180	42.3	180	22 AAF44071	DNA encoding a hum
8	173.8	40.8	1007	20 AAZ25531	pGR2PL3 cDNA seque
9	171.2	40.2	356	20 AAZ25537	Plasmid pGR2PL6 DN
10	129.4	30.4	180	20 AAZ25533	Receptor binding p
11	129.4	30.4	180	22 AAF44070	DNA encoding a rat

12	122.8	28.8	126	20	AAZ25542	Human ligand PCR p
13	120.8	28.4	180	20	AAZ25532	Porcine ligand (1-
14	120.8	28.4	180	22	AAF44069	DNA encoding a pig
15	119.2	28.0	567	22	AAF44065	BFGF (human fibrob
16	119.2	28.0	567	22	AAF44067	BFGF (human fibrob
17	119.2	28.0	567	22	AAF44068	BFGF (human fibrob
18	56.4	13.2	98	20	AAZ25526	Rat galanin recept
19	56.4	13.2	98	22	AAF44077	Nested PCR primer
20	56.4	13.2	98	22	AAZ25527	Rat galanin recept
21	51.6	12.1	98	22	AAF44078	Nested PCR primer
22	46	10.8	575	13	AAO28890	Sequence encoding
23	46	10.8	740	13	AAO27236	DNA encoding human
24	39.6	9.3	672	21	AAZ88387	Rat galanin cDNA n
25	38.4	9.0	3616	17	AAZ16858	Nitric oxide synth
26	38.4	9.0	4089	17	AAZ16857	Bovine endothelial
27	36	8.5	751	22	AAH04852	Human cDNA clone (
28	36	8.5	2568	22	AAH14623	Human cDNA sequenc
29	36	8.5	2924	22	AAF30484	Human protein phos
30	36	8.5	2981	22	AAF93820	Human cDNA encodin
31	36	8.5	2981	22	AAF29348	Human proliferation
32	36	8.5	6863	21	AAZ74847	Human ORFX ORF402
33	35.4	8.3	7800	21	AAZ20842	Human multiple tar
34	35.4	8.3	7800	21	AAZ34720	Human adenosine re
35	35.4	8.3	7803	20	AAZ55272	Human adenosine Al
36	35.4	8.3	114955	20	AAZ53491	Human receptor-rel
37	35.4	8.3	117609	21	AAZ21435	Endothelial nitrog
38	35.2	8.3	4097	16	AAO94255	Human 16405 DNA.
39	34.8	8.2	2040	22	AAZ31561	Human T-type volta
40	34.8	8.2	6132	20	AAZ83489	Human protein enco
41	33.2	7.8	1906	22	AAH99792	Human polynucleoti
42	33.2	7.8	1906	22	AAZ161254	Human neuronal acti
43	33.2	7.8	1925	20	AAZ32308	Human G protein-co
44	33.2	7.8	3517	22	AAH41182	Human G protein-co
45	33.2	7.8	4289	19	AAZ62147	HSV-2 strain SB5 C

ALIGNMENTS

RESULT 1

AAD04547

ID AAD04547 standard; cDNA; 426 BP.

XX AAD04547;

XX AC

XX 17-JUL-2001 (first entry)

XX DE Galanin family protein, novel human protein (NHP) cDNA #1.

XX DE Human; neurotropic; neuroprotective; antimicrobial; antiinflammatory;

XX KW analgesic; anorectic; antianorectic; therapy; novel human protein; NHP;

XX KW galanin; drug screening; physiological disorder; body weight regulation;

XX KW behaviour modulation; pain; inflammation; neuronal repair;

XX KW Alzheimer's dementia; inflammatory bowel disease; ss.

XX OS Homo sapiens.

XX FH Key

XX CDS Location/Qualifiers

FT 1..426

FT /\*tag= a

FT /product= "Novel human protein (NHP) #1 which share

FT sequence similarity with galanin proteins"

FT 1..96

FT /\*tag= b

FT 97..423

FT /\*tag= c

FT /product= "Mature novel human protein (NHP) #1"

XX WO200127273-A1.

XX PD 19-APR-2001.

XX PF 10-OCT-2000; 2000WO-US27922.











CC The present invention describes peptides (I) binding to galanin receptor  
CC proteins. (I) contain the sequence APAHRGGG or one substantially  
CC identical to it, and their precursors, salts, amides and esters, which  
CC bind especially to rat galanin receptor proteins. Products from the  
CC present invention are used in assays of galanin/galanin receptor binding  
CC and the development of drugs acting on galanin binding, such as memory  
CC function improvers, appetite improvers, and function regulators for the  
CC womb, kidney, prostate, testis or skeletal muscle. AAY45129 to AAY45154  
CC and AA225518 to AA225552 represent sequences used in the exemplification  
CC of the present invention.

XX Sequence 180 BP; 39 A; 57 C; 47 G; 37 T; 0 other;

Query Match 30.4%; Score 129.4; DB 20; Length 180;  
Best Local Similarity 84.8%; Pred. No. 7.3e-27;  
Matches 145; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 133 gcacctgcccacgggacgagggctggaccctcaatagtgctggtacctcttggt 132  
Db 133 gcacctgcccacgggacgagggctggaccctcaatagtgctggtacctcttggt 60  
QY 133 ccggtctccaccttcccccaatgggtgaccaaagcaggaagagagacagcccttgag 192  
Db 61 cctgtctccaccttctctcaaaaggccaccagggcaggaagacagctcagctcttgag 120  
QY 193 atctagacctgtggaagccatgatgggtccctccctactccaccctccca 243  
Db 121 atctagacctgtggaagccatgatgggtccctccctactccaccctccca 171

RESULT 11  
AAAF44070  
ID AAFA44070 standard; DNA; 180 BP.

XX AAF44070;  
XX 23-MAR-2001 (first entry)

XX DNA encoding a rat physiologically active protein.

XX Physiologically active protein; galanin receptor; GALR; FGF;  
KW fibroblast growth factor; ds.

XX Rattus sp.

XX JP2000270871-A.

XX 03-OCT-2000.

XX 24-MAR-1999; 99JP-0080303.

XX 24-MAR-1999; 99JP-0080303.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX WPI; 2001-019315/03.

XX Preparation of a new physiologically active peptide having a cleaved  
PT cysteine residue as N-terminal -

PS Disclosure; Page 35-36; 44pp; Japanese.

XX This invention relates to a method for the preparation of a  
CC physiologically active peptide having a cleaved cysteine residue at the  
CC end N-terminal, and has any of the amino acid sequences given in  
CC AAB65131 - AAB65136. The invention includes sequences AAB65137 - AAB65153  
CC which represent proteins related to the main proteins of the invention,  
CC including galanin receptors, and basic fibroblast growth factor. DNA  
CC sequences AAF44065 - AAF44071 and PCR primers AAF44072 - AAF44086 are  
CC used in the isolation and characterisation of DNA encoding the proteins  
CC of the invention.

SQ Sequence 180 BP; 39 A; 57 C; 47 G; 37 T; 0 other;

Query Match 30.4%; Score 129.4; DB 22; Length 180;  
Best Local Similarity 84.8%; Pred. No. 7.3e-27;  
Matches 145; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 73 gcacctgcccacgggacgagggctggaccctcaatagtgctggtacctcttggt 132  
Db 1 gcacctgcccacgggacgagggctggaccctcaatagtgctggtacctcttggt 60  
QY 133 ccggtctccaccttcccccaatgggtgaccaaagcaggaagagagagcccttgag 192  
Db 61 cctgtctccaccttctctcaaaaggccaccagggcaggaagacagctcagctcttgag 120  
QY 193 atctagacctgtggaagccatgatgggtccctccctactccaccctccca 243  
Db 121 atctagacctgtggaagccatgatgggtccctccctactccaccctccca 171

RESULT 12  
AAZ25542  
ID AAZ25542 standard; DNA; 126 BP.

XX AAZ25542;

XX 21-DEC-1999 (first entry)

XX Human ligand PCR product.

XX Physiologically active peptide; receptor binding; galanin receptor;  
KW GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin;  
KW drug development; memory function; appetite improver; womb; kidney;  
KW function regulator; prostate; testis; skeletal muscle; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9948920-A1.

XX 30-SEP-1999.

XX 24-MAR-1999; 99WO-JP01482.

XX 25-MAR-1998; 98JP-0078139.

XX 21-SEP-1998; 98JP-0266972.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Ohtaki T, Matsui H, Ishibashi Y, Ogi K, Kitada C;

XX WPI; 1999-572170/48.

XX Peptides binding to galanin receptor proteins, used to, e.g. improve  
PT kidney functioning -

XX Example 19; Page 90-91; 153pp; Japanese.

XX The present invention describes peptides (I) binding to galanin receptor  
CC proteins. (I) contain the sequence APAHRGGG or one substantially  
CC identical to it, and their precursors, salts, amides and esters, which  
CC bind especially to rat galanin receptor proteins. Products from the  
CC present invention are used in assays of galanin/galanin receptor binding  
CC and the development of drugs acting on galanin binding, such as memory  
CC function improvers, appetite improvers, and function regulators for the  
CC womb, kidney, prostate, testis or skeletal muscle. AAY45129 to AAY45154  
CC and AA225518 to AA225552 represent sequences used in the exemplification  
CC of the present invention.

XX Sequence 126 BP; 30 A; 35 C; 36 G; 25 T; 0 other;

Query Match 28.8%; Score 122.8; DB 20; Length 126;





Mon Mar 4 11:27:00 2002

```

RESULT 15
AAF44065
ID AAF44065 standard; DNA; 567 BP.
XX
AC AAF44065;
XX
DT 23-MAR-2001 (first entry)
XX
DE bFGF (human fibroblast growth factor) DNA sequence SEQ ID 15.
XX
KW Physiologically active protein; galanin receptor; GALR; FGF;
KW fibroblast growth factor; ds.
XX
OS Homo sapiens.
XX
PN JP2000270871-A.
XX
PD 03-OCT-2000.
XX
PF 24-MAR-1999; 99JP-0080303.
XX
PR 24-MAR-1999; 99JP-0080303.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
DR WPI; 2001-019315/03.
XX
PT Preparation of a new physiologically active peptide having a cleaved
PT cysteine residue as N-terminal
XX
PS Disclosure; Page 7; 44pp; Japanese.
XX
CC This invention relates to a method for the preparation of a
CC physiologically active peptide having a cleaved cysteine residue at the
CC end N-terminal, and has any of the amino acid sequences given in
CC AAB65131 - AAB65136. The invention includes sequences AAB65137 - AAB65153
CC which represent proteins related to the main proteins of the invention,
CC including galanin receptors, and basic fibroblast growth factor. DNA
CC sequences AAF44065 - AAF44071 and PCR primers AAF44072 - AAF44086 are
CC used in the isolation and characterisation of DNA encoding the proteins
CC of the invention.
XX
SQ Sequence 567 BP; 134 A; 153 C; 163 G; 117 T; 0 other;

Query Match 28.0%; Score 119.2; DB 22; Length 567;
Best Local Similarity 78.9%; Pred. No. 7.3e-24;
Matches 142; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 73 gcaactgccaccgggagcgagggtggtgacccctcaatagtggtggtacattcttggt 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 388 gtcctcggtccacagggcgaggaggtggtgacccctcaatagtggtggtacattcttggt 447
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 133 cccgtctccacctcccaaatgggtgaccaagagcggaagagggagagcccttgag 192
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 448 cccgtactccatccctccaggggtgaaaggagggaggaagagagagccctcggc 507
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 193 atcctagacctgtgaaaggccatcgatgggtccctccatccacccctccacagccctcc 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 508 atcctggacctgtgaaaggccatcgatgggtccctccatccacccctccacagccctcc 567
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Search completed: March 2, 2002, 23:56:26  
Job time: 5947 sec



Mon Mar 4 11:27:00 2002

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: March 2, 2002, 20:57:26 ; Search time 75 Seconds  
(without alignments)  
1286.395 Million cell updates/sec

Title: US-09-689-911-1\*  
Perfect score: 426  
Sequence: 1 atggctccctccctcgctccc.....aagatgtcctgaagtcataag 426

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues  
Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
1: /cgn2.6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2.6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2.6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2.6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2.6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	10.8	575	1	US-08-507-016-8
2	45.4	10.7	7218	1	US-08-232-463-14
3	38.4	9.0	4089	1	US-07-908-245-1
4	35.2	8.3	4097	3	US-09-123-708-5
5	35.2	8.3	4097	3	US-09-123-624-5
6	32	7.5	216	2	US-08-327-307-3
7	32	7.5	216	3	US-09-385-947-3
8	31.2	7.3	4403765	4	US-09-103-840A-2
9	31.2	7.3	4411529	4	US-09-103-840A-1
10	31	7.3	540	4	US-09-318-739A-1
11	31	7.3	540	4	US-08-147-592A-3
12	30.8	7.2	2272	4	US-09-007-005-3
13	30.4	7.1	277	4	US-09-244-796-3
14	30.4	7.1	2180	1	US-07-918-314-3
15	30.4	7.1	2900	1	US-07-918-314-5
16	30.4	7.1	2143	2	US-08-656-177A-1
17	30.2	7.1	2143	3	US-09-256-797-1
18	30.2	7.1	3603	1	US-08-188-582-15
19	30.2	7.1	3603	1	US-08-646-715-15
20	30.2	7.1	4897	6	5196516-7
21	30.2	7.1	36741	4	US-09-301-665-3
22	30.2	7.0	534	3	US-09-000-630C-26
23	30	7.0	534	3	US-08-862-730C-26
24	29.4	6.9	287	1	US-08-594-031-70
25	29.4	6.9	548	4	US-09-370-253-13
26	29.4	6.9	1045	2	US-08-773-231-13
27	29.4	6.9			

28	29.4	6.9	1086	2	US-08-773-251-14	Sequence 14, Appl
29	29.4	6.9	2253	2	US-08-773-251-12	Sequence 12, Appl
30	29.4	6.9	2803	2	US-08-773-251-8	Sequence 8, Appl
31	29.4	6.9	2807	2	US-08-773-251-7	Sequence 7, Appl
32	29.4	6.9	2959	2	US-08-773-251-1	Sequence 1, Appl
33	29.4	6.9	7218	1	US-08-232-463-14	Sequence 14, Appl
34	29.4	6.9	8802	3	US-08-896-449A-1	Sequence 1, Appl
35	29.4	6.9	8802	3	US-09-132-652-1	Sequence 1, Appl
36	29.2	6.9	289	4	US-09-007-005-17	Sequence 17, Appl
37	29.2	6.9	289	4	US-09-244-796-3	Sequence 17, Appl
38	29.2	6.9	375	4	US-09-240-274-77	Sequence 77, Appl
39	29.2	6.9	375	4	US-09-240-274-89	Sequence 89, Appl
40	29.2	6.9	375	4	US-09-240-274-90	Sequence 90, Appl
41	29.2	6.9	375	4	US-09-240-274-91	Sequence 91, Appl
42	29.2	6.9	3618	4	US-09-042-353-224	Sequence 224, App
43	29.2	6.9	3618	4	US-08-758-417A-72	Sequence 72, App
44	29.2	6.9	3699	1	US-08-053-131-120	Sequence 120, App
45	29.2	6.9	3699	1	US-08-645-641-120	Sequence 120, App

ALIGNMENTS

RESULT 1  
US-08-507-016-8  
; Sequence 8, Application US/08507016  
; Patent No. 5756460  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, HELEN F.  
; APPLICANT: SHINE, JOHN  
; TITLE OF INVENTION: HUMAN GALANIN, CDNA CLONES ENCODING  
; TITLE OF INVENTION: HUMAN GALANIN AND A METHOD OF PRODUCING HUMAN GALANIN  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ  
; STREET: 555 THIRTEENTH STREET, N.W.  
; CITY: WASHINGTON  
; STATE: D. C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/507,016  
; FILING DATE: 25-JULY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/108,733  
; FILING DATE: 03-SEP-1993  
; APPLICATION NUMBER: PCT/AU92/00097  
; FILING DATE: 06-MAR-1992  
; APPLICATION NUMBER: AU PK4953  
; FILING DATE: 06-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, BARBARA G.  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1871-117A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)783-6040  
; TELEFAX: (202)783-6031  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 575 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; HYPOTHETICAL: NO  
; FEATURE:  
; NAME/KEY: CDS

Query Match 10.7%; Score 45.4; DB 1; Length 7218;  
Best Local Similarity 1.5%; Pred. No. 0.00051;

CELL TYPE: Endothelial  
US-07-908-245-1









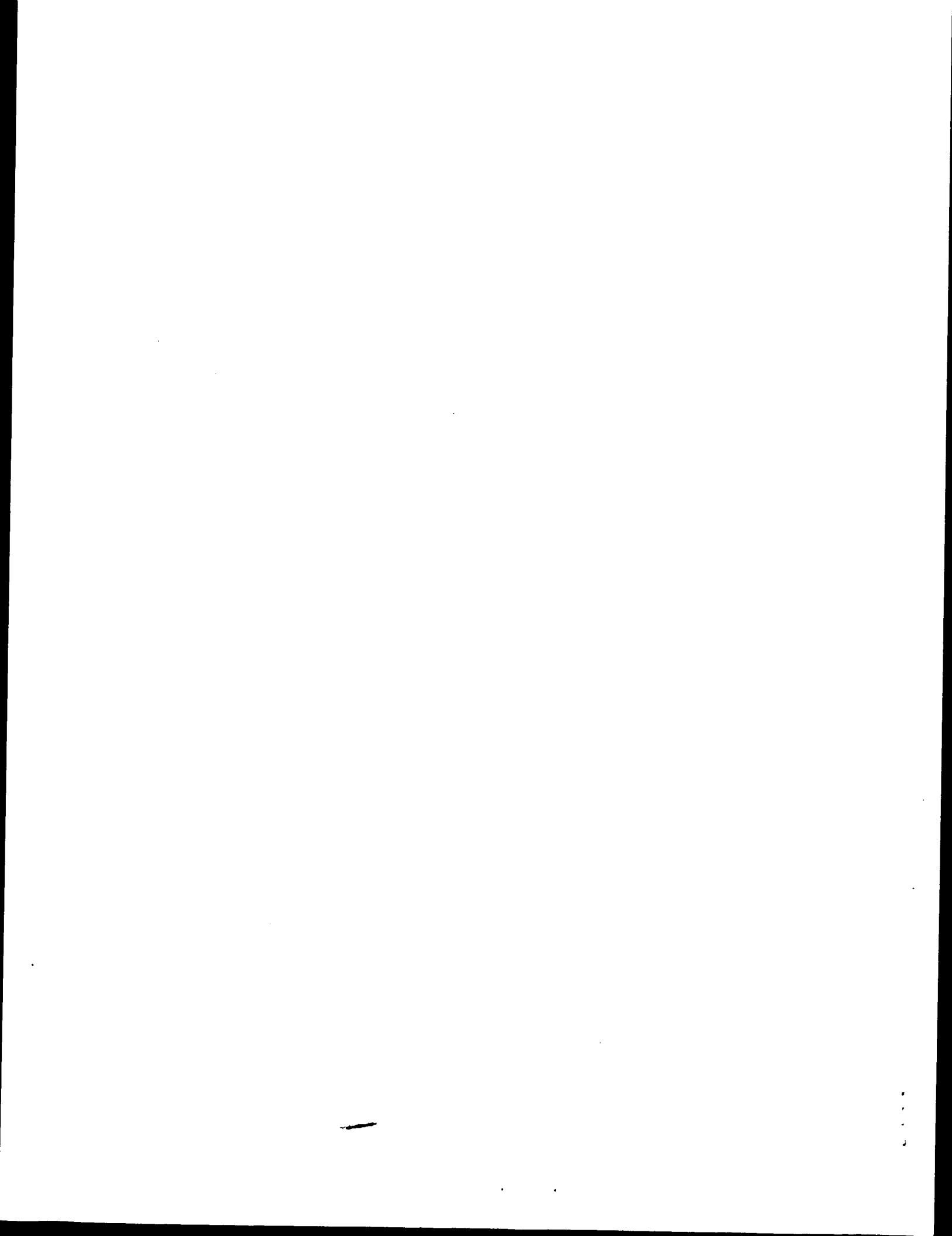


```

SEQUENCE CHARACTERISTICS:
LENGTH: 2180 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: intron
LOCATION: 1..29
FEATURE:
NAME/KEY: exon
LOCATION: 30..2125
FEATURE:
NAME/KEY: CDS
LOCATION: 32...616
;
US-07-918-314-3
Query Match 7.1%; Score 30.4; DB 1; Length 2180;
Best Local Similarity 51.5%; Pred. No. 9;
Matches 70; Conservative 66; Indels 0; Gaps 0;
QY 202 ctgtggaaggccatgatggctccctactccacccctccacagccctccaaagagaat 261
|||||
Db 762 CTGTGGGTATCTTCAGAGCCTCCCCCATGCCCCCAACAGCCACCTGGGCAGG 703
|||||
QY 262 gtgatggagacgtttgtccaaaccagagattggaggtaaacccaggaaacacagaagag 321
|||||
Db 702 CTCAGGGAGACCCCTGGGACACGGGCATGTGAGGACTGGACTGAGACCCCACTGGATGT 643
|||||
QY 322 acaccgacagagagag 337
|||||
Db 642 GGGCTGTTGGGAGCGG 627
|||||

```

Search completed: March 3, 2002, 00:28:23  
Job time: 12657 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2002, 20:57:21 ; Search time 1465.35 Seconds  
(without alignments)  
4795.986 Million cell updates/sec

Title: US-09-689-911-1  
Perfect score: 426  
Sequence: 1 atgctctctccctccgccc.....agatgtcctgaagtcataag 426

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenBank:

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_om.\*
- 20: em\_or.\*
- 21: em\_ov.\*
- 22: em\_pat.\*
- 23: em\_ph.\*
- 24: em\_pl.\*
- 25: em\_ro.\*
- 26: em\_sts.\*
- 27: em\_sy.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htgo\_hum.\*
- 31: em\_htgo\_inv.\*
- 32: em\_htgo\_rod.\*
- 33: em\_htg\_hum.\*
- 34: em\_htg\_inv.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	426	100.0	426	6	AX112343 Sequence
2	296.4	69.6	351	6	AX112345 Sequence
3	296.4	69.6	947	9	AF188492 Homo sapi
4	294.8	69.2	947	9	AF188493 Homo sapi
5	184.2	43.2	974	4	AF188490 Sus scrofa
6	183.6	43.1	694	10	AF188491 Rattus no
7	155.4	36.5	164824	2	AC023887 Homo sapi
8	153.8	36.1	100110	9	AC011506 Homo sapi
9	88.4	20.8	200603	2	AC024580 Homo sapi
10	47	11.0	28199	5	AF013613 Fugu rubr
11	46	10.8	575	6	A28025 Human prepr
12	46	10.7	7218	6	AR009787 Sequence 14
13	45.4	10.2	675	4	I66494 Bovine prep
14	43.4	10.2	774	4	X12582 Pig preprog
15	41.4	9.7	774	4	M13826 Pig preprog
16	40	9.4	172896	2	AC092758 Papio cyn
17	39.8	9.3	229896	14	AF232689 Rat cytom
18	39.6	9.3	680	10	AF232689 Rat cytom
19	39.6	9.3	699	10	M18102 Rat galanin
20	39.6	9.3	162060	2	J03624 Rat galanin
21	39.4	9.2	162495	9	AC007515 Homo sapi
22	39.4	9.2	172328	2	AC009996 Homo sapi
23	39.4	9.2	175465	2	AC027233 Homo sapi
24	39.2	9.2	213532	9	AC009821 Homo sapi
25	39	9.2	99173	9	AC013458 Homo sapi
26	39	9.2	144870	2	AL139800 Human DNA
27	38.8	9.1	78785	10	AL136328 Mus muscu
28	38.6	9.1	231454	9	AF111168 Homo sapi
29	38.6	9.1	101334	2	AF004030 Oryza sat
30	38.6	9.1	192110	2	AF004070 Oryza sat
31	38.4	9.0	3738	4	M89952 Bos taurus
32	38.4	9.0	4089	6	I18807 Sequence 1
33	38.4	9.0	4096	4	M99057 Bovine nitr
34	38.4	9.0	206413	9	AL390816 Human chr
35	38.4	9.0	206616	2	AC090622 Homo sapi
36	38.2	9.0	85000	9	AC009772 Homo sapi
37	37.6	8.8	120393	2	AL357132 Homo sapi
38	37.4	8.8	141885	9	AP001038 Homo sapi
39	37.4	8.8	200254	9	AC034116 Mus muscu
40	37.4	8.8	340000	9	AP001732 Homo sapi
41	37.2	8.7	608	9	HUMBTRO
42	37.2	8.7	78347	2	AC022642 Homo sapi
43	37	8.7	111084	9	AC006486 Homo sapi
44	37	8.7	118183	2	AC090433 Chlamydom
45	37	8.7	120955	9	AC002310 Human Chr

## ALIGNMENTS

RESULT 1  
AX112343  
LOCUS AX112343 426 bp DNA  
DEFINITION Sequence 1 from Patent WO0127273.  
ACCESSION AX112343  
VERSION AX112343.1 GI:13939104  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 426)  
AUTHORS Turner,C.A., Donoho,G., Wang,X., Hilbun,E., Zambrowicz,B. and Sands,A.T.  
HUMAN GALANIN family proteins and polynucleotides encoding the same

TITLE Patent: WO 0127273-A 1 19-APR-2001;  
JOURNAL Lexicon Genetics Incorporated (US)  
FEATURES Location/Qualifiers  
1..426  
/organism="Homo sapiens"

[illegible]

61	actcagacatccgcaactgcccacgggagcagagagctggagccctcaatagtgtctggc	120
143	actcagacatccgcaactgcccacgggagcagagagctggagccctcaatagtgtctggc	202
121	tacctcttggtccctcgctcctccactctcccaaatgggtgaccgaagcggaaagaggag	180
203	taccttttgggtccgctcctccactctcccaaatgggtgaccgaagcggaaagaggag	262
181	acagcccttgagatcctcagacctgtggaagccatcgatggctccctactccacacct	240
263	acagcccttgagatcctcagacctgtggaagccatcgatggctccctactccacacct	322
241	ccacagccctcaagaggaatgtatggagacgctttgccaaaccagagattggaggtaaa	300
323	ccacagccctccacagggaatgtatggagacgctttgccaaaccagagattggaggtctg	382
301	gcagag	306
383	ggcatg	388

RESULT	4
AF188493	PRI
LOCUS	947 bp mRNA
DEFINITION	Homo sapiens clone pGRHL02 galanin-like peptide precursor, mRNA, complete cds.
	24-DEC-1999

ACCESSION	AF188493
VERSION	AF188493.1
KEYWORDS	GI:6634715
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1 (bases 1 to 947) Ohtaki,T., Kumano,S., Ishibashi,Y., Ogi,K., Matsui,H., Harada,M., Kitada,C., Kurokawa,T., Onda,H. and Fujino,M.
TITLE	Isolation and cDNA cloning of a novel galanin-like peptide (GALP) from porcine hypothalamus
	from porcine hypothalamus
	274-282
	37041-37045 (1999)

J. Biol. Chem.	274	(22)	20069685
JOURNAL			
MEDLINE			
REFERENCE			
2 (bases 1 to 947)			
Authors	Ohtaki, T. and Kumano, S.		
TITLE	Direct Submission		
Submitted (21-Sep-1999)	Discovery Res. Labs. 1, Takeda Chemical		
Industries, Ltd., Wadai 10, Tsukuba, Ibaraki 300-4293, Japan			
Location/Qualifiers			
FEATURES			

```

1. 947
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="pGR2HL02"
83. 433
/note="neuropeptide"
/codon_start=1
/product="galanin-like peptide precursor"
/protein_id="AAF19725.1"
/db_xref="GI:6634716"
/translaton="MAPSPVLLVLLLSLAETPASAPHRGRGWTLSAGYI
PVLLHPQMGDDGKRETALEILDKKAIDGILPYSHPPQPSKRVNMMETFAKPEIGDI

```

BASE COUNT	LSMKIPKEEDVLKS	
ORIGIN		
246 a	241 c	212 g
		248 t

Query: Match 69.2% Score 294.8; DB 9; Length 947;

Query Match	97.7%	Pred. No. 3.1e-69;	0;	Gaps
Best Local Similarity	97.7%	0;	Mismatches 7;	Indels
Matches 299; Conservative				

**Qy**

1 atggtcctccctccgtagccccctgggcctcctcctcctcctccttctgtgagcctggcaag 60  
|||||  
**Qy**

D<sub>b</sub> 83 ATGGCTCCTCCCTCCGTCCTCCTCCTCGTCTCTTGCTGAGCCTGGCACAG 142  
c1 ccttcacccactccgagaccatccccacggaggagaggtggacctcaatagtctggc 120

[illegible]

143	ACTCCAGCATCCGACCTGCCCACCGGGGACGAGAGGCTGGACCCCTCAATAGTGTGCTGC	202
121	tacctttgggtcccgctccaccttcccacatgggtgaccagacgaaagagggag	180
203	TACCTTTCGGGTCCCGTCCCTCCACTTCCCANAATGGTGACCAAGACGGAAGAGGGAG	262
181	acagcccttgagatcctagacctgtgaaggccatcatggtgtccctactcccacct	240
263	ACAGCCCTTGAGATCTTAGACTGTGGAAGGCCATCGACGGGCTCCCTCTACTCCACCCCT	322
241	ccacagccctccagagaaatgtagtgagacgtttgccaaccagagatggaggtaaa	300
323	CCACAGCCCTCCCAAGGAATGTGATGGAGAGCTTGGCAACACAGAGATTGGAGATCTG	382
301	gcagag	306
383	GGCATG	388

[illegible]

VERSION AF188490.1 GI:6634709  
KEYWORDS  
SOURCE pig.  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Artiodactyla; Suina; Suidae; Sus.

REFERENCE  
Mammalia: Eutheria; 1 (bases 1 to 974)  
Ohtaki, T., Kumano, S., Ishibashi, Y., Ogi, K., Matsui, H., Harada, M.,  
Kitada, C., Kurokawa, T., Onda, H., and Fujino, M.  
Isolation and cDNA cloning of a novel galanin-like peptide (GALP)  
from porcine hypothalamus  
J. Biol. Chem. 274 (52), 37041-37045 (1999)

JOURNAL OF CLIMATE  
MEDLINE  
20069685  
REFERENCE  
2 (bases 1 to 974)

**AUTHORS** Ontaki, T. and Kumano, S.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (21-SEP-1999) Discovery Res. Labs. 1, Takeda Chemical  
Discovery Res. Labs. 1, Takeda Chemical  
Takeshi 200-4203 Japan

FEATURES	Location/Qualifiers
SOURCE	1. 974

```

source
/organism="Sus scrofa"
/db_xref="taxon:9823"
25_207

```

```

33. 3397
CDS
    /note="neuropeptide"
    /codon_start=1
    /translation="..."

```

```

/product="galanin-like peptide precursor"
/protein_id="AAFI9722.1"
/db_xref="GI:6634710"

```

```
/translation="MALTVPLIVLAVLLSLMESPASAPVHRGKGWILNSAGILDFG  
LHPPSRAEAGGKGKTLGILDLWKAIDGLPYQSQLASKRSLGETFAKPDGSGVTFVG  
DQVVDKPRIPGTRFOI"
```

BASE COUNT ORIGIN	258 a	278 c	229 g	209 t
ADDITIONAL COUNT	258 a	278 c	229 g	209 t

Query Match 43.2%; Score 184.2; DB 4; Length 974;

Best Local Similarity	68.5%;	Pred. No. 2.5e-39;	
Matches 272; Conservative		0; Mismatches 118;	Indels
			7; Gaps

Qy 29 tctctcctgtctctctgtgagcctgagagagatccagcatccgacacctgccacggg 88  
Qy tctctcctgtctctctgtgagcctgagagagatccagcatccgacacctgccacggg 88

[illegible]

Db 117 GGCGAGGAGGCTGGACCCCTCAACAGTGTGGTTACCTCCTGGTCCGTACTCCATCCGC 176

QY 149 cccaaatgggtgaccaaagacggaagagagagacaccccttgagatcctagacctgtgga 208



Mon Mar 4 11:27:00 2002

\* 34576 47285: contig of 12710 bp in length  
 \* 47286 47385: gap of unknown length  
 \* 47386 72370: contig of 24885 bp in length  
 \* 72371 72370: gap of unknown length  
 \* 72371 97221: contig of 24851 bp in length  
 \* 72371 97221: gap of unknown length  
 \* 97222 164824: contig of 67503 bp in length.  
 \* 97322 Location/Qualifiers

FEATURES  
 source  
 1. .164824  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="19"  
 /clone="RP11-541M19"  
 misc\_feature  
 1. .2092  
 /note="assembly\_name:Contig9  
 clone\_end:T7  
 vector\_side:right"

misc\_feature  
 2193. .7044  
 /note="assembly\_name:Contig10"  
 misc\_feature  
 7145. .19499  
 /note="assembly\_name:Contig11"  
 misc\_feature  
 19600. .34475  
 /note="assembly\_name:Contig12"  
 misc\_feature  
 34576. .47285  
 /note="assembly\_name:Contig13"  
 misc\_feature  
 47386. .72270  
 /note="assembly\_name:Contig14"  
 misc\_feature  
 72371. .97221  
 /note="assembly\_name:Contig15  
 clone\_end:SP6  
 vector\_side:right"  
 misc\_feature  
 97322. .164824  
 /note="assembly\_name:Contig16"

BASE COUNT 38305 a 41699 c 42797 g 41321 t 702 others  
 ORIGIN

Query Match 36.5%; Score 155.4; DB 2; Length 164824;  
 Best Local Similarity 96.4%; Pred. No. 1e-31;  
 Matches 159; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 215 tcgatgggtccctactccaccctccacagccctcccaagaggaatgtatgagacgt 274  
 Db 87746 TAGATGGGCTCCCTACTCTCCACCCCTCCACAGCCCTCCCAAGAGGAATGTATGGAGACGT 87805  
 QY 275 ttgccaaacacagagattggaggttaagccaggaaacacagagagacacccgacagag 334  
 Db 87806 TTGCCAAACACAGAGATTGGAGGTAAGCCAGGAAACACAGAGAGACACCCGACAGGAG 87865  
 QY 335 agggggaacaggaagtggcaggcagagcttagaggtctgggca 379  
 Db 87866 AGGGGGAACAAGGAAGTGGCAGGAGAGCTTAGAGGGTAAAGGAA 87910

RESULT 8  
 AC011506 100110 bp DNA PRI 21-APR-2000  
 LOCUS Homo sapiens chromosome 19 clone CTD-2086L14, complete sequence.  
 DEFINITION  
 AC011506  
 AC011506.3 GI:7630361  
 VERSION  
 HG.  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
 TITLE Direct Submission  
 JOURNAL Unpublished  
 REFERENCE  
 1 (bases 1 to 100110)  
 2 (bases 1 to 100110)  
 AUTHORS DOE Joint Genome Institute.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint

REFERENCE  
 3 (bases 1 to 100110)  
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-APR-2000) DOE Joint Genome Institute, 2800 Mitchell  
 Drive, Walnut Creek, CA 94598, USA  
 COMMENT On Apr 21, 2000 this sequence version replaced gi:6910529.  
 Draft Sequence Produced by DOE Joint Genome Institute  
 www.jgi.doe.gov  
 Finishing Completed at Stanford Human Genome Center  
 www.shgc.stanford.edu  
 Quality: Phrap Quality >=40 99.9% of Sequence;  
 Estimated Total Number of Errors is 0.2.  
 STS Content:  
 WT-11903 G21646.

FEATURES  
 source  
 1. .100110  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="19"  
 /clone="CTD-2086L14"  
 BASE COUNT 26449 a 23149 c 22857 g 27655 t  
 ORIGIN

Query Match 36.1%; Score 153.8; DB 9; Length 100110;  
 Best Local Similarity 95.8%; Pred. No. 2.8e-31;  
 Matches 158; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 215 tcgatgggtccctactccaccctccacagccctcccaagaggaatgtatgagacgt 274  
 Db 735 TAGACGGGCTCCCTACTCTCCACCCCTCCACAGCCCTCCCAAGAGGAATGTATGGAGACGT 794  
 QY 275 ttgccaaacacagagattggaggttaagccaggaaacacagagagacacccgacagag 334  
 Db 795 TTGCCAAACACAGAGATTGGAGGTAAGCCAGGAAACACAGAGAGACACCCGACAGGAG 854  
 QY 335 agggggaacaggaagtggcaggcagagcttagaggtctgggca 379  
 Db 855 AGGGGGAACAAGGAAGTGGCAGGAGAGCTTAGAGGGTAAAGGAA 899

RESULT 9  
 AC024580 200603 bp DNA HTG 20-APR-2001  
 LOCUS Homo sapiens chromosome 19 clone CTD-262117, WORKING DRAFT  
 DEFINITION  
 AC024580  
 AC024580.4 GI:13699641  
 VERSION  
 HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 AUTHORS DOE Joint Genome Institute.  
 TITLE Sequencing of Human Chromosome 19  
 JOURNAL Unpublished  
 REFERENCE  
 1 (bases 1 to 200603)  
 2 (bases 1 to 200603)  
 AUTHORS DOE Joint Genome Institute.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 COMMENT On Apr 20, 2001 this sequence version replaced gi:9954666.  
 -----Genome Center  
 Center: Joint Genome Institute  
 Center Code: JGI  
 Web site: http://www.jgi.doe.gov  
 -----  
 Project Information  
 Center Project Name: 836654, BC801678  
 Center clone name: C1TB\_E1\_262117  
 -----









[illegible]

RESULT 15

PIGPGAL 774 bp mRNA MAM 27-APR-1993  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 pig adrenal gland, cDNA to mRNA, clones pGAL5A2, pGAL8B2.  
 Sus scrofa  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 1 (bases 1 to 774)  
 Roekaeus, A. and Brownstein, M.J.  
 Construction of a porcine adrenal medullary cDNA library and  
 nucleotide sequence analysis of two clones encoding a galanin  
 precursor  
 Proc. Natl. Acad. Sci. U.S.A. 83, 6287-6291 (1986)  
 86313566 Location/Qualifiers  
 1..774  
 /organism="Sus scrofa"  
 /db\_xref="taxon:9823"  
 228..599  
 /note="preprogalanin"  
 /codon\_start=1  
 /protein\_id="AAA31097.1"  
 /db\_xref="GI:164606"  
 /translation="MPRGKALLSALLSALSATLGLSPVKEKRGWTLNSAGYLLG  
 PHAIDNHRSPHDYGYGLAGKRELEPEDEARPGGFDRLQSDKAIRTIMEFLAFLHKEA  
 GALGRILGFLPSAASSEDAGQS"  
 324..414  
 /note="galanin"  
 /db\_xref="taxon:9823"  
 415..774  
 /note="galanin"  
 mat\_peptide 141 a 281 c 222 g 130 t  
 BASE COUNT  
 ORIGIN

[illegible]

```
Search completed: March 2, 2002, 23:54:07
Job time: 10606 sec
```



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2002, 20:31:41 ; Search time 1494.43 Seconds  
(without alignments)  
3063.176 Million cell updates/sec

Title: US-09-689-911-1  
Perfect score: 426  
Sequence: 1 atggtctctcctccgcccc.....aagatgctctgaagtcataag 426

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estfun:  
2: em\_esthum:  
3: em\_estlin:  
4: em\_estom:  
5: em\_estpl:  
6: em\_estba:  
7: em\_estro:  
8: em\_estov:  
9: em\_hic:  
10: gb\_estl:  
11: gb\_est2:  
12: gb\_hic:  
13: gb\_gss:  
14: em\_gss\_fun:  
15: em\_gss\_hum:  
16: em\_gss\_inv:  
17: em\_gss\_pln:  
18: em\_gss\_pro:  
19: em\_gss\_rod:  
20: em\_gss\_vrt:  
21: em\_gss\_other:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	150.6	35.4	565	13	AQ549952
2	123.6	29.0	465	13	AW416677
3	99.2	23.3	304	10	AW436648
4	46	10.8	727	10	AL556408
5	46	10.8	804	10	AL556409
6	44.4	10.4	760	11	BI255627
7	42.2	9.9	499	10	AL504892
8	42.2	9.9	712	10	BE060480
9	41.8	9.8	934	11	BG176001
10	41.6	9.8	420	10	AV836850
11	41.6	9.8	541	10	AL502174
12	41.6	9.8	919	13	CNS00655

BF254655 HVSMEf000  
W83304 mf24d03.r1  
W75493 mf55b12.r1  
AI894042 mg89g12.y  
AZ753635 RPCI-24-1  
AL513663 RPCI-11-1  
AL108460 Drosophil  
BE964354 601658055  
BF551196 UI-R-CO-h  
AW141500 EST291550  
AL053013 Drosophil  
AA016654 mg89g12.f  
AL074613 Drosophil  
AL060767 Drosophil  
AL108238 Drosophil  
AK019070 Mus muscu  
AQ937099 NB1-607R  
BE403648 WHE0435\_A  
AL187533 Tetraodon  
AW175662 RC3-BF004  
AL056652 Drosophil  
BE967163 601661043  
BI249086 602992416  
BF527076 602039994  
AL066307 Drosophil  
AL076960 Drosophil  
BF344055 602016865  
BF680503 602155222  
BB534299 BB534299  
AL030478 Fugu rubr  
AL077527 Drosophil  
AL055013 Drosophil  
AL277084 Tetraodon

# ALIGNMENTS

RESULT 1  
AQ549952 565 bp DNA GSS 28-MAY-1999  
LOCUS RPCI-11-418L8.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-418L8,  
DEFINITION DNA sequence.  
ACCESSION AQ549952  
VERSION AQ549952.1 GI:4909129  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 565)  
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter  
J.C.  
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready  
Map Building  
JOURNAL Unpublished (1997)  
COMMENT Other\_GSSs: RPCI-11-418L8.TV  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbeetigr.org  
Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong  
(pieterdejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from  
Research Genet cs (info@resgen.com). BAC end search page:  
http://www.tigr.org/tldb/humgen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: SP6  
Class: BAC ends.  
Location/Qualifiers

# FEATURES



```

RESULT 5
AL556409 804 bp mRNA EST 16-FEB-2001
AL556409 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DK004YA08 5
prime, mRNA sequence.
AL556409
AL556409.1 GI:12899058
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 804)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .804
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DK004YA08"
/tissue_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/notes="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 174 a 261 c 211 g 156 t 2 others
ORIGIN

Query Match 10.8%; Score 46; DB 10; Length 804;
Best Local Similarity 59.0%; Pred. No. 0.45;
Matches 79; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 1 atgggtctctccgtccccctggctctctctctctctctgtgctgagcgtggcagag 60
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 227 ATGGCCGAGGAGGAGCGCCCTCTGTGCTGCCCTCCCTCCCTCCGCGCGGCCCTTCTGCC 286
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 61 actcagatcgcacacctgccaccgagcagagagcgtggaccctcaatagtgtggc 120
|| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 287 TGTGGGGGCTCTGTGTCGCCGCCAAGGAAACGAGGCTGGACCTGAACACGCGGGC 346
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 121 tacctctgggtcc 134
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 347 TACCTGCTGGGCC 360

RESULT 6
BI255627 760 bp mRNA EST 17-JUL-2001
LOCUS NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5115887 5',
DEFINITION mRNA sequence.
ACCESSION BI255627
VERSION BI255627.1 GI:14809207
KEYWORDS EST.
SOURCE human.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 760)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
TITILE
AUTHORS
REFERENCE

```









100

1

\_\_\_\_\_





```

105 rgArgGluThrProThrGlyGluGlyGluGlnGlySerGlyArgGlnSer 121
1472 GAAGAGAGACACGACAGGAGAGGGGGAACATGGAAGTGGCAGCAGAGC 521
122 LeuGluAspLeuGly 126
522 TTACAGGGTAAAGGA 536
seq_name: gb_est1:AW416677

seq_documentation_block:
LOCUS AW416677 465 bp mRNA EST 09-JUL-2000
DEFINITION 52226 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION AW416677
VERSION AW416677.1 GI:6944559
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 465)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
JOURNAL EST discovery in swine
COMMENT Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Plate: 24 row: B column: 13
Seq primer: ATTAGGTGACACTATAG.
FEATURES
source
1. .465
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT 80 a 155 c 133 g 97 t
ORIGIN
alignment_scores:
Quality: 248.50 Length: 68
Ratio: 4.212 Gaps: 1
Percent Similarity: 86.765 Percent Identity: 73.529
alignment_block:
US-09-689-911-2 x AW416677
Align seg 1/1 to: AW416677 from: 1 to: 465
5 ServValProLeuValLeuValLeuValLeuLeuSerLeuAlaGluTh 21
81 ACTGTCCTCTGATGCTTCTGAGTC...CTGCTCAGCCTGATGGATC 127
21 rProAlaSerAlaProAlaHisArgGlyArgGlyClyTrpThrLeuAsn 38
128 TCCAGCCTCTGCTCCGTCACAGGGGCGAGGAGGCTGGACCTCAACA 177

```

```

38 erAlaClyTyrLeuLeuGlyProValLeuHisLeuProGlnMetGlyAsp 54
178 GTGCTGGTTACCTCTCGGGTCCGCTACTCCATCCGCCCTCCAGGGCTGAA 227
55 GlnAspGlyLysArgGluThrAlaLeuGluLeuAspLeuTrpLysAl 71
228 GGAGGGGGAAGGGGAGACAGCCCTCGGGATCTGGACCTGTGGAAGGC 277
71 aile 72
|||||
278 CATT 281

```

seq\_name: gb\_est1:AW436648

```

seq_documentation_block:
LOCUS AW436648 304 bp mRNA EST 09-JUL-2000
DEFINITION 77047 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION AW436648
VERSION AW436648.1 GI:6971954
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 304)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
JOURNAL EST discovery in swine
COMMENT Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Plate: 32 row: F column: 8
Seq primer: ATTAGGTGACACTATAG.
FEATURES
Location/Qualifiers
1. .304
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT 57 a 99 c 92 g 56 t
ORIGIN
alignment_scores:
Quality: 204.50 Length: 58
Ratio: 4.090 Gaps: 1
Percent Similarity: 86.207 Percent Identity: 70.690
alignment_block:
US-09-689-911-2 x AW436648
Align seg 1/1 to: AW436648 from: 1 to: 304
5 ServValProLeuValLeuValLeuLeuSerLeuAlaGluTh 21
132 ACTGTCCCTCTGATGCTTCTTGAGTC...CTGCTCAGCCTGATGGAGTC 178

```

[illegible]

seq_name	gb_est1:AW141500	seq_documentation_block:	498 bp	mRNA	EST	30-OCT-1999
LOCUS	AW141500					
DEFINITION	EST291550	Normalized rat embryo,				
		Bento Soares				
		Rattus sp.				
		cdna clone				
		sequence.				

ACCESSION  
AW141500  
VERSION  
AW141500.1 GI:6161294  
KEYWORDS  
EST.  
SOURCE  
Rattus sp.  
ORGANISM  
Rattus sp.  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE  
1 (bases 1 to 498)  
Lee,N.H., Glodok A., Chandra,I., Mason,T.M., Quackenbush,J.,  
Kerlavage,A.R. and Adams,M.D.  
Rat Genome Project: Generation of a Rat EST (EST) Catalog & Rat  
Gene Index

Unpublished (1998)  
Contact: Lee, NH  
The Institute for Genomic Research  
9712, Medical Center Drive, Rockville, MD 20850, USA  
Tel: (301)-838-3529  
Fax: (301)-838-0208  
Email: nhlee@tigr.org  
For clone availability, additional sequence and expression  
information related to this EST please check the TIGR Rat Gene  
Index (<http://www.tigr.org/tdb/rgi/rgi.html>). To order a clone  
contact the ATCC (<http://www.atcc.org/atcc.html>).  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1. .498  
/organism="Rattus sp."

```

BASE COUNT
ORIGIN
105 a 160 c 137 g 95 t
/notes=vector: pN7Tpac: Site_1: EcoRI; Site_2: NotI"
/dev_stage="embryo 8, 12, 18 dpc"
/clone_lib="Normalized rat embryo, Bento Soares"
/clone="RG1BW81"
/db_xref="taxon:10118"

```

[illegible]

195 CCTGTCAGCCACTCTGGGGCTCGGGATGCCCAACAAGGAGAAGAGAGGCT 244

alignment\_scores:  
 Quality: 104.50 Length: 116  
 Ratio: 1.560 Gaps: 3  
 Percent Similarity: 57.759 Percent Identity: 31.034

alignment\_block:  
 US-09-689-911-2 x W83304 ..

Align seg 1/1 to: W83304 from: 1 to: 629

1 MetAlaProProSerValProLeuValLeuValLeuLeuLeuLeu 17  
 140 ATGGCCAGAGGATGGTTATCTCTAGCTGGCTGCTCTGTTGTGAC 189  
 17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34  
 190 CTGTGACCACTCTGGGACATGGGATGCTGCAAGAGAGAGAGAGGTT 239  
 34 rpThrLeuAsnSerAlaGlyTyrLeuLeuGlyPro.....ValLeuHis 48  
 240 GGACCCCTGAACAGGCTGGCTACCTCTGCGCCACATGCCATTGCACAC 289  
 49 LeuProGlnMetGlyAspGln.....AspGlyLysArgGluThrAl 62  
 290 CACAGATCATTTAGCGACACAGCTGGCTCACAGGCAAGAGGAGTTACA 339  
 62 aLeuGluLeuLeuAspLeuThrLysAlaHisArgGlyLeuProTyrSerH 79  
 340 ACTGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 385  
 79 isProGlnProSerLysArgAsnValMetGluThrPheAlaLysPro 95  
 386 ..CTGAGACACATTTGTCGCGCTATATATGAGTTCCTCAGTTCTTG 433  
 96 GluLeuGlyLysAlaArgLysHisArgGlyLeuThrProThrGly 111  
 434 CACCTTAAAGCGCGGCGCTCGACACCTGCTGGCCTGCTGGCCTGGC 481

seq\_name: gb\_est1:AI894042

seq\_documentation\_block:  
 LOCUS AI894042 679 bp mRNA EST 15-MAR-2000  
 DEFINITION mg89g12.y1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA  
 clone IMAGE:440230 5' similar to gb:M77440 GALANIN PRECURSOR (HUMAN  
 ); gb:L38580 Mus musculus galanin gene (MOUSE); mRNA sequence.  
 ACCESSION AI894042 GI:5599944  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 679)  
 Marra.M., Hillier.L., Kucaba.T., Martin.J., Beck.C., Wylie.T.,  
 Underwood.K., Steptoe.M., Theising.B., Allen.M., Bowers.Y., Person  
 B., Swaller.T., Gibbons.M., Pape.D., Harvey.N., Schurk.R., Ritter  
 E., Kohn.S., Shin.T., Jackson.Y., Cardenas.M., McCann.R.,  
 Waterston.R. and Willson.R.  
 The WashU-NCI Mouse EST Project 1999  
 Unpublished (1999)  
 Other\_ESTs: mg89g12.x1  
 Contact: Marra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 This read is a RESEQUENCE of a previously sequenced mouse clone.  
 This read has been verified (found to hit its original self in the

correct orientation)  
 MG1:265566  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 402.  
 FEATURES  
 source  
 1..679  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:440230"  
 /clone\_lib="Soares mouse embryo NbME13.5 14.5"  
 /sex="unknown"  
 /tissue\_type="embryo"  
 /dev\_stage="13.5-14.5dpc total fetus"  
 /lab\_host="DH10B"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
 was primed with a Not I - oligo(dT) primer [5',  
 TGTTACCAATCTAGTGGAGGCGCGGAAATTTTCTTTTCTTTTCTTTT  
 T 3'], on equal amounts of mRNA from 2 13.5dpc and 2  
 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne  
 State Univ., from 2 ]; double-stranded cDNA was ligated to  
 Eco RI adaptors (Pharmacia), digested with Not I and  
 cloned into the Not I and Eco RI sites of the modified  
 pT7T3 vector. Library went through one round of  
 normalization, and was constructed by Bento Soares and  
 M.Fatima Bonaldo."

BASE COUNT 158 a 188 c 176 g 156 t 1 others  
 ORIGIN

alignment\_scores:  
 Quality: 104.50 Length: 95  
 Ratio: 1.833 Gaps: 3  
 Percent Similarity: 60.000 Percent Identity: 35.789

alignment\_block:  
 US-09-689-911-2 x AI894042 ..

Align seg 1/1 to: AI894042 from: 1 to: 679

1 MetAlaProProSerValProLeuValLeuValLeuLeuLeuLeu 17  
 130 ATGGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 179  
 17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34  
 180 CTGTGACCACTCTGGGACATGGGATGCTGCAAGAGAGAGAGAGGTT 229  
 34 rpThrLeuAsnSerAlaGlyTyrLeuLeuGlyPro.....ValLeuHis 48  
 230 GGACCCCTGAACAGGCTGGCTACCTCTGCGCCACATGCCATTGCACAC 279  
 49 LeuProGlnMetGlyAspGln.....AspGlyLysArgGluThrAl 62  
 280 CACAGATCATTTAGCGACACAGCTGGCTCACAGGCAAGAGGAGTTACA 329  
 62 aLeuGluLeuLeuAspLeuThrLysAlaHisArgGlyLeuProTyrSerH 79  
 330 ACTGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 375  
 79 isProGlnProSerLysArgAsnValMetGlu 90  
 376 ..CTGAGACACATTTGTCGCGCTATATATGAGGAG 408

seq\_name: gb\_est1:AL556408

seq\_documentation\_block:  
 LOCUS AL556408 727 bp mRNA EST 16-FEB-2001  
 DEFINITION AL556408 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CS0DK004YA08 3  
 prime, mRNA sequence.  
 ACCESSION AL556408  
 VERSION AL556408.1 GI:128999056



us-09-689-911-2-1st

Mon Mar 4 11:27:02 2002

```

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 727)
JOURNAL Li.W.B., Gruber,C., Jesse,J. and Polayes,D.
COMMENT Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..727
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DK004YA08"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/notes="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 133 a 203 c 254 g 133 t
ORIGIN
4 others

alignment_scores:
Quality: 104.50 Length: 91
Ratio: 2.010 Gaps: 5
Percent Similarity: 57.143 Percent Identity: 42.857

alignment_block:
US-09-689-911-2 x AL556408/rev ..
Align seg 1/1 to reverse of: AL556408 from: 1 to: 727

10 LeuLeuLeuValLeuLeuSerLeuAlaGluThrProAlaSerAla... 25
481 CTCCTGCTCGCTCCCTCTCTCTCGCGCGCCCTTTCTGCTCTCGCGG 432
26 .....ProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerA 39
431 GCTCTGGTGGCGCGCCAGGAAAACGA...GGCTGGACCCCTGAACAGC 385
39 laGlyTyrLeuLeuGlyPro.....ValLeuHisLeuProGlnMetGly 53
381 CGGGTACCTGCTGGGCCACATCGGTTGGCAACACAGGTCATTTCAGC 335
54 AspGlnAspGly.....LysArgGluThrAlaLeuGluLeuLeuAs 67
334 GACAGAATGGCTCACCAGTAAGCGGAGCTCGGCCCGGAA..... 293
67 pLeuTrpLysAlaIleAspGlyLeuProTyrSerHisProGlnProS 84
292 .....GATGACATGAACACAGGAAAGCTTTGACAGGTCCATT 256
84 erLysArgAsnValMetGluThr 91
255 CTGAACAATATATCATCGGCACA 233

seq_name: gb_est2:BI255627

seq_documentation_block:
LOCUS BI255627 760 bp mRNA EST 17-JUL-2001
DEFINITION 602976496F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5115887 5',

```

```

mRNA sequence.
BI255627
BI255627.1 GI:14809207
EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 760)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11281 row: o column: 24
High quality sequence stop: 645.
Location/Qualifiers
1..760
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5115887"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/notes="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
BASE COUNT 172 a 233 c 202 g 133 t
ORIGIN

alignment_scores:
Quality: 103.50 Length: 91
Ratio: 1.917 Gaps: 6
Percent Similarity: 59.341 Percent Identity: 41.758

alignment_block:
US-09-689-911-2 x BI255627 ..
Align seg 1/1 to: BI255627 from: 1 to: 760

10 LeuLeuValLeuLeuSerLeuAlaGluThrProAlaSerAla... 25
183 CTCCTTCTCGCTCCCTCTCTCTCGCGCGCCCTTTCTGCTCTGCGGG 232
26 .....ProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerA 39
233 GCTCTGGTGGCGCCAGGAAAACGA...GGCTGGACCCCTGAACAGC 279
39 laGlyTyrLeuLeuGlyPro.....ValLeuHisLeuProGlnMetGly 53
280 CGGGTACCTGCTGGGCCACATCGCTTGGCAACACAGTCATTTCAGC 329
54 AspGlnAspGly.....LysArgGluThrAlaLeuGluLeuLeuAs 67
330 GACAAGAATGGCTCACCAGCAGGAGCTCGCGCCGGAAGATGACATG 379
67 pLeuTrpLysAlaIleAspGlyLeuProTyrSerHisProGlnProS 84
380 AACCAGGAGCTTTGACAGT...CCATAC.....C 408
84 erLysArgAsnValMetGluThr 91
409 GTGAACAATATATCATCGGCACA 431

```

seq\_name: gb\_est2:BF551196

seq\_documentation\_block:

LOCUS BF551196 423 bp mRNA EST 12-DEC-2000  
 DEFINITION UI-R-CO-hw-a-05-0-UI.r1 UI-R-CO Rattus norvegicus cDNA clone  
 UI-R-CO-hw-a-05-0-UI 5', mRNA sequence.

ACCESSION BF551196

VERSION BF551196.1 GI:11660926

KEYWORDS EST.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 423)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene  
 discovery

Genome Res. 6 (9), 791-806 (1996)

JOURNAL 97044477

MEDLINE

COMMENT

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Fax: 319 335 8250

Tel: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

cDNA Library Preparation: M.B. Soares Lab Clone distribution:

clones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.E. Consortium at

LLNL (info@image.llnl.gov). IMAGE ID= 1773887

Seq primer: M13 Forward.

FEATURES

Source

Location/Qualifiers

1..423

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="UI-R-CO-hw-a-05-0-UI"

/clone\_lib="UI-R-CO"

/dev\_stage="adult"

/lab\_host="DH10B (Life Technologies)"

/note="Vector: pT7D-Pac (Pharmacia) with a modified

polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-CO

library is a subtracted library derived from the UI-R-Al

and UI-R-E1 libraries. The UI-R-Al library consisted of a

mixture of individually tagged normalized libraries

constructed from rat placenta, adult lung, brain, liver,

kidney, heart, spleen, ovary, and muscle. The UI-R-E1

library consisted of a mixture of individually tagged

normalized libraries constructed from 8, 12 and 18-day

embryo. The tag is a string of 3-5 nucleotides present

between the Not I site and the oligo-dT track which

allows identification of the library of origin of a clone

within the mixture. The subtracted library (UI-R-CO) was

constructed as follows: PCR amplified cDNA inserts from a

pool of UI-R-Al and UI-R-E1 clones from which 3' ESTs had

been derived was used as a driver in a hybridization with

the pooled UI-R-Al and UI-R-E1 library in the form of

single-stranded circles. The remaining single-stranded

circles (subtracted library) was purified by

hydroxyapatite column chromatography, converted to

double-stranded circles and electroporated into DH10B

bacteria (Life Technologies) to generate the UI-R-CO

library. This procedure has been previously described

(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,

1996)."

BASE COUNT 96 a 128 c 114 g 82 t 3 others

ORIGIN

alignment\_scores:

Quality: 100.50

Ratio: 1.827

Length: 100

Gaps: 5

Percent Similarity: 55.000 Percent Identity: 37.000

alignment\_block:

US-09-689-911-2 x BF551196 ..

Align seg 1/1 to: BF551196 from: 1 to: 423

```

1  MetAlaProProSerValProLeuValLeuLeuValLeuLeuLeuSe 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
107 ATGCCAGGGGCGAGCTTATCTCTGCTAGCTGCTCTCTGTTGTTGCAAC 156
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 rLeuAlaGluHrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
157 CCTGTACGCCACTCTGGGGCTCGGATGCAACAAAGAGAGATAGAGGCT 206
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 rPrThrLeuAsnSerAlaGlyTyrLeuLeuGlyProValLeuHis 48
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
207 GGACCTGAACAGCGCTGCTACCTCTGGGCCCA.....CATGCCATT 250
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
49 .....LeuProGlnMetGlyAspGlnAspGlyLys 59
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 GACAAACACAGCATTTATCGAAGCATGCG...CTCACAGGCAAGAG 297
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
59 gGluThrAlaLeuGluLeuLeuAsp.....LeuTrpLysAlaLeuAspG 74
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
298 GGAGTTACCACTGAAGTGGAGGAGGAGACTANGAAGTGTCTGTGTGN 347
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
74 lyLeuProTyrSerHisProProGlnProSerLysArgAsnValMetGlu 90
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
348 CCCTGCTGAGAGCAAT.....ATCGTCCGCACCTATATATGAG 385
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

seq\_name: gb\_est2:W75493

seq\_documentation\_block:

LOCUS W75493 642 bp mRNA EST 20-JUN-1996  
 DEFINITION me55b12.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA  
 clone IMAGE:391391 5' similar to gb:M77140 GALANIN PRECURSOR (HUMAN  
 ); gb:L38580 Mus musculus galanin gene (MOUSE);, mRNA sequence.

ACCESSION W75493

VERSION W75493.1 GI:1385709

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 642)

REFERENCE

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
 Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.

TITLE The WashU-HMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:243223

Seq primer: ETPrimer

High quality sequence stop: 342.

Location/Qualifiers

1..642

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:391391"

/clone\_lib="Soares mouse embryo NbME13.5 14.5"

/sex="unknown"



**AUTHORS** Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

**TITLE** Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

**JOURNAL** Unpublished

**REFERENCE** 2 (bases 1 to 745)

**AUTHORS** Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

**TITLE** Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

**JOURNAL** Unpublished

**REFERENCE** 3 (bases 1 to 745)

**AUTHORS** Genoscope.

**TITLE** Direct Submission

**JOURNAL** Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

**COMMENT** This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

**FEATURES** Location/Qualifiers

source

1..745

/organism="Tetraodon nigroviridis"

/db\_xref="taxon:99883"

/clone="064A13"

/clone\_lib="G"

/note="Genoscope sequence ID : C0BG064AA07LP1-end : T7"

BASE COUNT 172 a 185 c 228 g 157 t 3 others

ORIGIN

alignment\_scores:

Quality: 98.00 Length: 113

Ratio: 1.750 Gaps: 5

Percent Similarity: 49.558 Percent Identity: 31.858

alignment\_block:

US-09-689-911-2 x CNS03WDO/rev ..

Align seg 1/1 to reverse of: CNS03WDO from: 1 to: 745

3 ProProSerValProLeuValLeuLeuValLeuLeuSerLeuAl 19

||||| ||| ||||| :||| :||| :||| :|||

306 CCTCTTCTCTCCCTCCAGGCGAGTGTCTCAACCTGTCTGCTATCTGC 257

19 aGluThrProAlaSerAlaProAlaHisArgGlyArgGlyTrpThrL 36

| ||||| :||| :||| :||| :||| :||| :|||

256 AGCAACCCCTCAGGCAATACCTGTCTCAACGCTCTCCACGCGCGAGCTG 207

36 euAnSerAlaGlyTrpLeuLeuGlyProVal...LeuHisLeuProGln 51

||||| ||||| ||| |||

206 TGCAGCCA.....GGCCCTGTGCGCCTTCCACGCGCGCTG 172

52 MetGlyAspGlnAspGlyLysArgGluThrAlaLeuGluLeuAspLe 68

||||| ||||| ||| |||

171 CCAGCGCAGGACCGGACACGA..... 148

68 uTrpLysAlaLeuAspGlyLeuProTyrSerHisProGlnProSerL 85

||||| ||||| :||| :||| :||| :|||

141 .....GGTCTACCTGACCTGAACCCCTCAGGCACACACC 114

85 ysArgAsnValMetGluThrPheAlaLysProGluLeuGlyGlyLysAla 101

||||| :||| :||| :||| :|||

113 ATCAGCAG.....CCGACGCGGAGCGCGGAGGTGAGCGG 79

102 ArgLysHisArg...ArgGluThrProThrGlyGlyGly 113

||||| ||||| :||| :||| :||| :|||

78 AGACCTGGGAGGCCGACACAGTCCAGGCTGGGCGCGGA 40

seq\_name: gb\_est1:AI385770

seq\_documentation\_block:

**LOCUS** AI385770 559 bp mRNA EST 27-JAN-1999

**DEFINITION** mg89q12.x1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:440230 3' similar to gb:U38580 Mus musculus galanin gene (MOUSE);, mRNA sequence.

**ACCESSION** AI385770

**VERSION** AI385770.1 GI:4199233

**KEYWORDS** EST.

**SOURCE** house mouse.

**ORGANISM** Mus musculus

**REFERENCE** 1 (bases 1 to 559)

**AUTHORS** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

**TITLE** The WashU-NCI Mouse EST Project 1999

**JOURNAL** Unpublished (1999)

**COMMENT** Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information. MGI:265566

This clone was previously sequenced on the 5' end only, this new data is from the 3' end

High quality sequence stop: 433.

**FEATURES** Location/Qualifiers

1..559

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:440230"

/clone\_lib="Soares mouse embryo NbME13.5 14.5"

/sex="unknown"

/tissue.type="embryo"

/dev\_stage="13.5-14.5dpc total fetus"

/lab\_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 137 a 142 c 131 g 149 t

ORIGIN

alignment\_scores:

Quality: 97.50 Length: 95

Ratio: 1.773 Gaps: 5

Percent Similarity: 57.895 Percent Identity: 35.789

alignment\_block:

US-09-689-911-2 x AI385770/rev ..

Align seg 1/1 to reverse of: AI385770 from: 1 to: 559

1 MetAlaProSerValProLeuValLeuLeuValLeuLeuLeu 17

||||| :||| :||| :||| :||| :|||

559 ATGGCAGAGCAGCGATCTCTGCTAGCTGCTCTTG...GTTGTGAC 513

17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34

[illegible]

library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering.bac.htm>)  
or from Research Genetics (<http://www.htsc.washington.edu>). BAC end Web Server:  
<http://www.htsc.washington.edu>  
Plate: 1077 row: E column: 5  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 850.

# FEATURES

Location/Qualifiers  
1. .850  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="Plate=1077 Col=5 Row=E"  
/clone\_lib="RPCI-11 Human Male BAC Library"  
/sex="male"  
/note="Vector: pBACE3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRI Methylase. Size selected DNA was cloned into the  
pBACE3.6 vector at EcoRI sites"

BASE COUNT 158 a 244 c 419 g 8 t 21 others  
ORIGIN

## alignment\_scores:

Quality: 93.50 Length: 123  
Ratio: 1.612 Gaps: 9  
Percent Similarity: 47.154 Percent Identity: 32.520

## alignment\_block:

US-09-689-911-2 x AQ743759 ..

Align seg 1/1 to: AQ743759 from: 1 to: 850

```

19 AlaGluThrProAlaSerAlaPro.....AlaHisArgL 30
||||| |||||:|||||
345 GCCGACGCCGCCGCCACGCCGCCGACCAACGAGCGCGCGGGCGG 394
30 yArgGlyGlyTrpThrLeuAsnSerAlaGlyTyrLeuLeuGly..... 44
||||| ||||| |||
395 CAGGGCGGGGCCACCCACGAGCAGCGGGA.....GGCAGAGGC 435
45 .....ProValLeuHisLeuPro.....Gln 51
||| ||| |||
436 GGGAGCGCGCGCCGCCACACGCCGCCGCGCGCGCGGGAAGAGAG 485
52 MetGlyAspGlnAspGlyLysArgGluThrAlaLeuGluLeuLeuAspLe 68
|||||:||||| ||||| ||| |||
486 CCAGGGAGCGAGACGGCGCGCGCGCGCGCGCGGAG..... 524
68 uTrpLysAlaIleAspGlyLeuProTyrSerHisProGln..... 82
||||| |
525 .....GACGGGAGC.....CCCCGCGAGGGGGCG 549
83 ..ProSerLysArgAsnValMetGluThrPheAlaLysProGluIleGly 98
|||: |||||
550 CACCGAGCGCGGAAC.....GGC 569
99 GlyLysAlaArgLysHisArgGluThrProThrGly.GluGlyGluG 115
:|||||:||||| ||||| ||| |||:|||||
570 GCGGGGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 619
115 InGlySerGlyArgGln 120
||||| |||
620 AGGGCGGGGGCGCGCAG 636

```